

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
7 February 2002 (07.02.2002)

PCT

(10) International Publication Number
WO 02/10378 A2

- (51) International Patent Classification⁷: C12N 15/11, A61K 31/713
- (21) International Application Number: PCT/US01/23874
- (22) International Filing Date: 30 July 2001 (30.07.2001)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
09/629,644 31 July 2000 (31.07.2000) US
- (71) Applicant (*for all designated States except US*): ISIS PHARMACEUTICALS, INC. [US/US]; Carlsbad Research Center, 2292 Faraday Avenue, Carlsbad, CA 92008 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (*for US only*): COWSERT, Lex, M. [US/US]; 3008 Newshire Street, Carlsbad, CA 92008 (US). WYATT, Jacqueline [US/US]; 1065 Hymetus Avenue, Encinitas, CA (US). FREIER, Susan, M. [US/US]; 2946 Renault Street, San Diego, CA 92112 (US). MONIA, Brett, P. [US/US]; 7605 Nueva Castile Way, La Costa, CA 92009 (US). BUTLER, Madeline, M. [US/US]; 15951 Avenida Calma, Rancho Santa Fe, CA 92091 (US). MCKAY, Robert [US/US]; 277 Caminito Pescado #73, San Diego, CA 92116 (US).
- (74) Agents: BAK, Mary, E. et al.; Howson and Howson, Spring House Corporate Center, Box 457, Spring House, PA 19477 (US).
- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 02/10378 A2

(54) Title: ANTISENSE MODULATION OF PTP1B EXPRESSION

(57) Abstract: Compounds, compositions and methods are provided for modulating the expression of PTP1B. The compositions comprise antisense compounds, particularly antisense oligonucleotides, targeted to nucleic acids encoding PTP1B. Methods of using these compounds for modulation of PTP1B expression and for treatment of diseases associated with expression of PTP1B are provided.

ANTISENSE MODULATION OF PTP1B EXPRESSION

FIELD OF THE INVENTION

The present invention provides compositions and methods for modulating the expression of PTP1B. In particular, this invention relates to compounds, particularly antisense oligonucleotides, specifically hybridizable with nucleic acids encoding PTP1B. Such oligonucleotides have been shown to modulate the expression of PTP1B.

BACKGROUND OF THE INVENTION

The process of phosphorylation, defined as the attachment of a phosphate moiety to a biological molecule through the action of enzymes called kinases, represents one course by which intracellular signals are propagated resulting finally in a cellular response. Within the cell, proteins can be phosphorylated on serine, threonine or tyrosine residues and the extent of phosphorylation is regulated by the opposing action of phosphatases, which remove the phosphate moieties. While the majority of protein phosphorylation within the cell is on serine and threonine residues, tyrosine phosphorylation is modulated to the greatest extent during oncogenic transformation and growth factor stimulation (Zhang, *Crit. Rev. Biochem. Mol. Biol.*, 1998, 33, 1-52).

Because phosphorylation is such a ubiquitous process within cells and because cellular phenotypes are largely influenced by the activity of these pathways, it is currently believed that a number of disease states and/or disorders are a result of either aberrant activation of, or functional mutations in, kinases and phosphatases. Consequently, considerable attention has been devoted recently to the characterization of tyrosine kinases and tyrosine phosphatases.

PTP1B (also known as protein phosphatase 1B and PTPN1) is an endoplasmic reticulum (ER)-associated enzyme originally isolated as the major protein tyrosine phosphatase of the human placenta (Tonks et al., *J. Biol. Chem.*, 1988, 263, 6731-6737; Tonks et al., *J. Biol. Chem.*, 1988, 263, 6722-6730).

An essential regulatory role in signaling mediated by the insulin receptor has been established for PTP1B. PTP1B interacts with and dephosphorylates the activated insulin receptor both in vitro and in intact cells resulting in the downregulation of the

- 2 -

signaling pathway (Goldstein et al., *Mol. Cell. Biochem.*, 1998, 182, 91-99; Seely et al., *Diabetes*, 1996, 45, 1379-1385). In addition, PTP1B modulates the mitogenic actions of insulin (Goldstein et al., *Mol. Cell. Biochem.*, 1998, 182, 91-99). In rat adipose cells overexpressing PTP1B, the translocation of the GLUT4 glucose transporter was inhibited, implicating PTP1B as a negative regulator of glucose transport as well (Chen et al., *J. Biol. Chem.*, 1997, 272, 8026-8031).

5 Mouse knockout models lacking the PTP1B gene also point toward the negative regulation of insulin signaling by PTP1B. Mice harboring a disrupted PTP1B gene showed increased insulin sensitivity, increased phosphorylation of the insulin receptor and when placed on a high-fat diet, PTP1B $-\text{/}$ mice were resistant to weight gain and remained insulin sensitive (Elchebly et al., *Science*, 1999, 283, 1544-1548). These studies clearly establish PTP1B as a therapeutic target in the treatment of diabetes and obesity.

10 PTP1B, which is differentially regulated during the cell cycle (Schievella et al., *Cell. Growth Differ.*, 1993, 4, 239-246), is expressed in insulin sensitive tissues as two different isoforms that arise from alternate splicing of the pre-mRNA (Shifrin and Neel, *J. Biol. Chem.*, 1993, 268, 25376-25384). It was recently demonstrated that the ratio of the alternatively spliced products is affected by growth factors such as insulin and differs in various tissues examined (Sell and Reese, *Mol. Genet. Metab.*, 1999, 66, 189-192). In these studies it was also found that the levels of the variants correlated with the plasma insulin concentration and percentage body fat and may therefore be used as a biomarker for patients with chronic hyperinsulinemia or type 2 diabetes.

15 Liu and Chernoff have shown that PTP1B binds to and serves as a substrate for the epidermal growth factor receptor (EGFR) (Liu and Chernoff, *Biochem. J.*, 1997, 327, 139-145). Furthermore, in A431 human epidermoid carcinoma cells, PT1B was found to be inactivated by the presence of H_2O_2 generated by the addition of EGF. These studies indicate that PTP1B can be negatively regulated by the oxidation state of the cell, which is often deregulated during tumorigenesis (Lee et al., *J. Biol. Chem.*, 1998, 273, 15366-15372).

- 3 -

Overexpression of PTP1B has been demonstrated in malignant ovarian cancers and this correlation was accompanied by a concomitant increase in the expression of the associated growth factor receptor (Wiener et al., *Am. J. Obstet. Gynecol.*, 1994, 170, 1177-1183).

5 PTP1B has been shown to suppress transformation in NIH3T3 cells induced by the neu oncogene (Brown-Shimer et al., *Cancer Res.*, 1992, 52, 478-482), as well as in rat 3Y1 fibroblasts induced by v-srk, v-src, and v-ras (Liu et al., *Mol. Cell. Biol.*, 1998, 18, 250-259) and rat-1 fibroblasts induced by bcr-abl (LaMontagne et al., *Proc. Natl. Acad. Sci. U. S. A.*, 1998, 95, 14094-14099). It has also been shown that PTP1B
10 promotes differentiation of K562 cells, a chronic myelogenous leukemia cell line, in a similar manner as does an inhibitor of the bcr-abl oncoprotein. These studies describe the possible role of PTP1B in controlling the pathogenesis of chronic myeloid leukemia (LaMontagne et al., *Proc. Natl. Acad. Sci. U. S. A.*, 1998, 95, 14094-14099).

PTP1B negatively regulates integrin signaling by interacting with one or more
15 adhesion-dependent signaling components and repressing integrin-mediated MAP kinase activation (Liu et al., *Curr. Biol.*, 1998, 8, 173-176). Other studies designed to study integrin signaling, using a catalytically inactive form of PTP1B, have shown that PTP1B regulates cadherin-mediated cell adhesion (Balsamo et al., *J. Cell. Biol.*, 1998, 143, 523-532) as well as cell spreading, focal adhesion and stress fiber formation and
20 tyrosine phosphorylation (Arregui et al., *J. Cell. Biol.*, 1998, 143, 861-873).

Currently, therapeutic agents designed to inhibit the synthesis or action of PTP1B include small molecules (Ham et al., *Bioorg. Med. Chem. Lett.*, 1999, 9, 185-186; Skorey et al., *J. Biol. Chem.*, 1997, 272, 22472-22480; Taing et al., *Biochemistry*, 1999, 38, 3793-3803; Taylor et al., *Bioorg. Med. Chem.*, 1998, 6, 1457-1468; Wang et al., *Bioorg. Med. Chem. Lett.*, 1998, 8, 345-350; Wang et al., *Biochem. Pharmacol.*, 1997, 54, 703-711; Yao et al., *Bioorg. Med. Chem.*, 1998, 6, 1799-1810) and peptides (Chen et al., *Biochemistry*, 1999, 38, 384-389; Desmarais et al., *Arch. Biochem. Biophys.*, 1998, 354, 225-231; Roller et al., *Bioorg. Med. Chem. Lett.*, 1998, 8, 2149-2150). In addition, disclosed in the PCT publication WO 97/32595 are phosphopeptides and antibodies that inhibit the association of PTP1B with the activated
30

- 4 -

insulin receptor for the treatment of disorders associated with insulin resistance. Antisense nucleotides against PTP1B are also generally disclosed (Olefsky, 1997).

There remains a long felt need for additional agents capable of effectively inhibiting PTP1B function and antisense technology is emerging as an effective means 5 for reducing the expression of specific gene products. This technology may therefore prove to be uniquely useful in a number of therapeutic, diagnostic, and research applications for the modulation of PTP1B expression.

The present invention, therefore, provides compositions and methods for modulating PTP1B expression, including modulation of the alternatively spliced form 10 of PTP1B.

SUMMARY OF THE INVENTION

The present invention is directed to antisense compounds, particularly oligonucleotides, which are targeted to a nucleic acid encoding PTP1B, and which modulate the expression of PTP1B. Pharmaceutical and other compositions 15 comprising the antisense compounds of the invention are also provided. Further provided are methods of modulating the expression of PTP1B in cells or tissues comprising contacting said cells or tissues with one or more of the antisense compounds or compositions of the invention. Further provided are methods of treating an animal, particularly a human, suspected of having or being prone to a disease or 20 condition associated with expression of PTP1B by administering a therapeutically or prophylactically effective amount of one or more of the antisense compounds or compositions of the invention.

DETAILED DESCRIPTION OF THE INVENTION

The present invention employs oligomeric antisense compounds, particularly oligonucleotides, for use in modulating the function of nucleic acid molecules encoding PTP1B, ultimately modulating the amount of PTP1B produced. This is accomplished 25 by providing antisense compounds which specifically hybridize with one or more nucleic acids encoding PTP1B. As used herein, the terms "target nucleic acid" and

- 5 -

"nucleic acid encoding PTP1B" encompass DNA encoding PTP1B, RNA (including pre-mRNA and mRNA) transcribed from such DNA, and also cDNA derived from such RNA. The specific hybridization of an oligomeric compound with its target nucleic acid interferes with the normal function of the nucleic acid. This modulation of 5 function of a target nucleic acid by compounds which specifically hybridize to it is generally referred to as "antisense". The functions of DNA to be interfered with include replication and transcription. The functions of RNA to be interfered with include all vital functions such as, for example, translocation of the RNA to the site of protein translation, translation of protein from the RNA, splicing of the RNA to yield 10 one or more mRNA species, and catalytic activity which may be engaged in or facilitated by the RNA. The overall effect of such interference with target nucleic acid function is modulation of the expression of PTP1B. In the context of the present invention, "modulation" means either an increase (stimulation) or a decrease (inhibition) in the expression of a gene. In the context of the present invention, inhibition is the 15 preferred form of modulation of gene expression and mRNA is a preferred target.

It is preferred to target specific nucleic acids for antisense. "Targeting" an antisense compound to a particular nucleic acid, in the context of this invention, is a multistep process. The process usually begins with the identification of a nucleic acid sequence whose function is to be modulated. This may be, for example, a cellular gene 20 (or mRNA transcribed from the gene) whose expression is associated with a particular disorder or disease state, or a nucleic acid molecule from an infectious agent. In the present invention, the target is a nucleic acid molecule encoding PTP1B. The targeting process also includes determination of a site or sites within this gene for the antisense interaction to occur such that the desired effect, e.g., detection or modulation of 25 expression of the protein, will result. Within the context of the present invention, a preferred intragenic site is the region encompassing the translation initiation or termination codon of the open reading frame (ORF) of the gene. Since, as is known in the art, the translation initiation codon is typically 5'-AUG (in transcribed mRNA molecules; 5'-ATG in the corresponding DNA molecule), the translation initiation codon is also referred to as the "AUG codon," the "start codon" or the "AUG start 30

- 6 -

codon". A minority of genes have a translation initiation codon having the RNA sequence 5'-GUG, 5'-UUG or 5'-CUG, and 5'-AUA, 5'-ACG and 5'-CUG have been shown to function in vivo. Thus, the terms "translation initiation codon" and "start codon" can encompass many codon sequences, even though the initiator amino acid in each instance is typically methionine (in eukaryotes) or formylmethionine (in prokaryotes). It is also known in the art that eukaryotic and prokaryotic genes may have two or more alternative start codons, any one of which may be preferentially utilized for translation initiation in a particular cell type or tissue, or under a particular set of conditions. In the context of the invention, "start codon" and "translation initiation codon" refer to the codon or codons that are used in vivo to initiate translation of an mRNA molecule transcribed from a gene encoding PTP1B, regardless of the sequence(s) of such codons.

It is also known in the art that a translation termination codon (or "stop codon") of a gene may have one of three sequences, i.e., 5'-UAA, 5'-UAG and 5'-UGA (the corresponding DNA sequences are 5'-TAA, 5'-TAG and 5'-TGA, respectively). The terms "start codon region" and "translation initiation codon region" refer to a portion of such an mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (i.e., 5' or 3') from a translation initiation codon. Similarly, the terms "stop codon region" and "translation termination codon region" refer to a portion of such an mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (i.e., 5' or 3') from a translation termination codon.

The open reading frame (ORF) or "coding region," which is known in the art to refer to the region between the translation initiation codon and the translation termination codon, is also a region which may be targeted effectively. Other target regions include the 5' untranslated region (5'UTR), known in the art to refer to the portion of an mRNA in the 5' direction from the translation initiation codon, and thus including nucleotides between the 5' cap site and the translation initiation codon of an mRNA or corresponding nucleotides on the gene, and the 3' untranslated region (3'UTR), known in the art to refer to the portion of an mRNA in the 3' direction from

- 7 -

the translation termination codon, and thus including nucleotides between the translation termination codon and 3' end of an mRNA or corresponding nucleotides on the gene. The 5' cap of an mRNA comprises an N7-methylated guanosine residue joined to the 5'-most residue of the mRNA via a 5'-5' triphosphate linkage. The 5' cap region of an mRNA is considered to include the 5' cap structure itself as well as the first 50 nucleotides adjacent to the cap. The 5' cap region may also be a preferred target region.

Although some eukaryotic mRNA transcripts are directly translated, many contain one or more regions, known as "introns," which are excised from a transcript before it is translated. The remaining (and therefore translated) regions are known as "exons" and are spliced together to form a continuous mRNA sequence. mRNA splice sites, i.e., intron-exon junctions, may also be preferred target regions, and are particularly useful in situations where aberrant splicing is implicated in disease, or where an overproduction of a particular mRNA splice product is implicated in disease. Aberrant fusion junctions due to rearrangements or deletions are also preferred targets. It has also been found that introns can also be effective, and therefore preferred, target regions for antisense compounds targeted, for example, to DNA or pre-mRNA.

Once one or more target sites have been identified, oligonucleotides are chosen which are sufficiently complementary to the target, i.e., hybridize sufficiently well and with sufficient specificity, to give the desired effect.

In the context of this invention, "hybridization" means hydrogen bonding, which may be Watson-Crick, Hoogsteen or reversed Hoogsteen hydrogen bonding, between complementary nucleoside or nucleotide bases. For example, adenine and thymine are complementary nucleobases which pair through the formation of hydrogen bonds. "Complementary," as used herein, refers to the capacity for precise pairing between two nucleotides. For example, if a nucleotide at a certain position of an oligonucleotide is capable of hydrogen bonding with a nucleotide at the same position of a DNA or RNA molecule, then the oligonucleotide and the DNA or RNA are considered to be complementary to each other at that position. The oligonucleotide and the DNA or RNA are complementary to each other when a sufficient number of corresponding

- 8 -

positions in each molecule are occupied by nucleotides which can hydrogen bond with each other. Thus, "specifically hybridizable" and "complementary" are terms which are used to indicate a sufficient degree of complementarity or precise pairing such that stable and specific binding occurs between the oligonucleotide and the DNA or RNA target. It is understood in the art that the sequence of an antisense compound need not be 100% complementary to that of its target nucleic acid to be specifically hybridizable. An antisense compound is specifically hybridizable when binding of the compound to the target DNA or RNA molecule interferes with the normal function of the target DNA or RNA to cause a loss of utility, and there is a sufficient degree of complementarity to avoid non-specific binding of the antisense compound to non-target sequences under conditions in which specific binding is desired, i.e., under physiological conditions in the case of in vivo assays or therapeutic treatment, and in the case of in vitro assays, under conditions in which the assays are performed.

Antisense compounds are commonly used as research reagents and diagnostics. For example, antisense oligonucleotides, which are able to inhibit gene expression with exquisite specificity, are often used by those of ordinary skill to elucidate the function of particular genes. Antisense compounds are also used, for example, to distinguish between functions of various members of a biological pathway. Antisense modulation has, therefore, been harnessed for research use.

The specificity and sensitivity of antisense is also harnessed by those of skill in the art for therapeutic uses. Antisense oligonucleotides have been employed as therapeutic moieties in the treatment of disease states in animals and man. Antisense oligonucleotides have been safely and effectively administered to humans and numerous clinical trials are presently underway. It is thus established that oligonucleotides can be useful therapeutic modalities that can be configured to be useful in treatment regimes for treatment of cells, tissues and animals, especially humans.

In the context of this invention, the term "oligonucleotide" refers to an oligomer or polymer of ribonucleic acid (RNA) or deoxyribonucleic acid (DNA) or mimetics thereof. This term includes oligonucleotides composed of naturally-occurring nucleobases, sugars and covalent internucleoside (backbone) linkages as well as

- 9 -

oligonucleotides having non-naturally-occurring portions which function similarly. Such modified or substituted oligonucleotides are often preferred over native forms because of desirable properties such as, for example, enhanced cellular uptake, enhanced affinity for nucleic acid target and increased stability in the presence of
5 nuclease.

While antisense oligonucleotides are a preferred form of antisense compound, the present invention comprehends other oligomeric antisense compounds, including but not limited to oligonucleotide mimetics such as are described below. The antisense compounds in accordance with this invention preferably comprise from about 8 to
10 about 50 nucleobases (i.e. from about 8 to about 50 linked nucleosides). Particularly preferred antisense compounds are antisense oligonucleotides, even more preferably those comprising from about 12 to about 30 nucleobases. As is known in the art, a nucleoside is a base-sugar combination. The base portion of the nucleoside is normally a heterocyclic base. The two most common classes of such heterocyclic bases are the
15 purines and the pyrimidines. Nucleotides are nucleosides that further include a phosphate group covalently linked to the sugar portion of the nucleoside. For those nucleosides that include a pentofuranosyl sugar, the phosphate group can be linked to either the 2', 3' or 5' hydroxyl moiety of the sugar. In forming oligonucleotides, the phosphate groups covalently link adjacent nucleosides to one another to form a linear
20 polymeric compound. In turn the respective ends of this linear polymeric structure can be further joined to form a circular structure, however, open linear structures are generally preferred. Within the oligonucleotide structure, the phosphate groups are commonly referred to as forming the internucleoside backbone of the oligonucleotide. The normal linkage or backbone of RNA and DNA is a 3' to 5' phosphodiester linkage.

25 Specific examples of preferred antisense compounds useful in this invention include oligonucleotides containing modified backbones or non-natural internucleoside linkages. As defined in this specification, oligonucleotides having modified backbones include those that retain a phosphorus atom in the backbone and those that do not have a phosphorus atom in the backbone. For the purposes of this specification, and as
30 sometimes referenced in the art, modified oligonucleotides that do not have a

- 10 -

phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides.

Preferred modified oligonucleotide backbones include, for example, phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, 5 aminoalkylphosphotriesters, methyl and other alkyl phosphonates including 3'-alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, and boranophosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those having inverted polarity 10 wherein the adjacent pairs of nucleoside units are linked 3'-5' to 5'-3' or 2'-5' to 5'-2'. Various salts, mixed salts and free acid forms are also included.

Representative United States patents that teach the preparation of the above phosphorus-containing linkages include, but are not limited to, U.S.: 3,687,808; 4,469,863; 4,476,301; 5,023,243; 5,177,196; 5,188,897; 5,264,423; 5,276,019; 15 5,278,302; 5,286,717; 5,321,131; 5,399,676; 5,405,939; 5,453,496; 5,455,233; 5,466,677; 5,476,925; 5,519,126; 5,536,821; 5,541,306; 5,550,111; 5,563,253; 5,571,799; 5,587,361; and 5,625,050, certain of which are commonly owned with this application, and each of which is herein incorporated by reference.

Preferred modified oligonucleotide backbones that do not include a phosphorus atom therein have backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatom and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These include those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone 20 backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide 25 backbones; amide backbones; and others having mixed N, O, S and CH₂ component parts.

- 11 -

Representative United States patents that teach the preparation of the above oligonucleosides include, but are not limited to, U.S.: 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,264,562; 5,264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307; 5,561,225; 5,596,086; 5,602,240; 5,610,289; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623,070; 5,663,312; 5,633,360; 5,677,437; and 5,677,439, certain of which are commonly owned with this application, and each of which is herein incorporated by reference.

In other preferred oligonucleotide mimetics, both the sugar and the internucleoside linkage, i.e., the backbone, of the nucleotide units are replaced with novel groups. The base units are maintained for hybridization with an appropriate nucleic acid target compound. One such oligomeric compound, an oligonucleotide mimetic that has been shown to have excellent hybridization properties, is referred to as a peptide nucleic acid (PNA). In PNA compounds, the sugar-backbone of an oligonucleotide is replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone. Representative United States patents that teach the preparation of PNA compounds include, but are not limited to, U.S.: 5,539,082; 5,714,331; and 5,719,262, each of which is herein incorporated by reference. Further teaching of PNA compounds can be found in Nielsen et al., *Science*, 1991, 254, 1497-1500.

Most preferred embodiments of the invention are oligonucleotides with phosphorothioate backbones and oligonucleosides with heteroatom backbones, and in particular -CH₂-NH-O-CH₂-, -CH₂-N(CH₃)-O-CH₂- [known as a methylene (methylimino) or MMI backbone], -CH₂-O-N(CH₃)-CH₂-, -CH₂-N(CH₃)-N(CH₃)-CH₂- and -O-N(CH₃)-CH₂-CH₂- [wherein the native phosphodiester backbone is represented as -O-P-O-CH₂] of the above referenced U.S. patent 5,489,677, and the amide backbones of the above referenced U.S. patent 5,602,240. Also preferred are oligonucleotides having morpholino backbone structures of the above-referenced U.S. patent 5,034,506.

- 12 -

Modified oligonucleotides may also contain one or more substituted sugar moieties. Preferred oligonucleotides comprise one of the following at the 2' position: OH; F; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; O-, S- or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl may be substituted or unsubstituted C₁ to C₁₀ alkyl or C₂ to C₁₀ alkenyl and alkynyl. Particularly preferred are O[(CH₂)_nO]_mCH₃, 5 O(CH₂)_nOCH₃, O(CH₂)_nNH₂, O(CH₂)_nCH₃, O(CH₂)_nONH₂, and O(CH₂)_nON[(CH₂)_nCH₃]₂, where n and m are from 1 to about 10. Other preferred oligonucleotides comprise one of the following at the 2' position: C₁ to C₁₀ lower alkyl, substituted lower alkyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH₃, OCN, Cl, 10 Br, CN, CF₃, OCF₃, SOCH₃, SO₂CH₃, ONO₂, NO₂, N₃, NH₂, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an oligonucleotide, or a group for improving the pharmacodynamic properties of an oligonucleotide, and other substituents having 15 similar properties. A preferred modification includes 2'-methoxyethoxy (2'-O-CH₂CH₂OCH₃, also known as 2'-O-(2-methoxyethyl) or 2'-MOE) (Martin et al., *Helv. Chim. Acta*, 1995, 78, 486-504) i.e., an alkoxyalkoxy group. A further preferred modification includes 2'-dimethylaminoxyethoxy, i.e., a O(CH₂)₂ON(CH₃)₂ group, 20 also known as 2'-DMAOE, as described in examples hereinbelow, and 2'-dimethylaminoethoxyethoxy (also known in the art as 2'-O-dimethylaminoethoxyethyl or 2'-DMAEOE), i.e., 2'-O-CH₂-O-CH₂-N(CH₃)₂, also described in examples hereinbelow.

Other preferred modifications include 2'-methoxy (2'-O-CH₃), 2'-aminopropoxy (2'-OCH₂CH₂CH₂NH₂) and 2'-fluoro (2'-F). Similar modifications may also be made at 25 other positions on the oligonucleotide, particularly the 3' position of the sugar on the 3' terminal nucleotide or in 2'-5' linked oligonucleotides and the 5' position of 5' terminal nucleotide. Oligonucleotides may also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar. Representative United States patents that teach the preparation of such modified sugar structures include, but are not limited to, U.S.: 30 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786;

- 13 -

5,514,785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646,265; 5,658,873; 5,670,633; and 5,700,920, certain of which are commonly owned with the instant application, and each of which is herein incorporated by reference in its entirety.

5 Oligonucleotides may also include nucleobase (often referred to in the art simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified nucleobases include other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted 10 adenines and guanines, 5-halo particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine. Further nucleobases include those disclosed in United States Patent No. 3,687,808, those disclosed in *The Concise Encyclopedia Of Polymer Science And Engineering*, pages 858-859, Kroschwitz, J.I., ed. John Wiley & Sons, 1990, those disclosed by Englisch et al., *Angewandte Chemie*, International Edition, 1991, 30, 613, and those disclosed by Sanghvi, Y.S., Chapter 15, *Antisense Research and 15 Applications*, pages 289-302, Crooke, S.T. and Lebleu, B., ed., CRC Press, 1993. Certain of these nucleobases are particularly useful for increasing the binding affinity of 20 the oligomeric compounds of the invention. These include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and O-6 substituted purines, including 2-aminopropyl-adenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2°C (Sanghvi, Y.S., 25 Crooke, S.T. and Lebleu, B., eds., *Antisense Research and Applications*, CRC Press,

- 14 -

Boca Raton, 1993, pp. 276-278) and are presently preferred base substitutions, even more particularly when combined with 2'-O-methoxyethyl sugar modifications.

Representative United States patents that teach the preparation of certain of the above noted modified nucleobases as well as other modified nucleobases include, but 5 are not limited to, the above noted U.S. 3,687,808, as well as U.S.: 4,845,205; 5,130,302; 5,134,066; 5,175,273; 5,367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,594,121, 5,596,091; 5,614,617; and 5,681,941, certain of which are commonly owned with the instant application, and each of which is herein incorporated by reference, and United States 10 patent 5,750,692, which is commonly owned with the instant application and also herein incorporated by reference.

Another modification of the oligonucleotides of the invention involves chemically linking to the oligonucleotide one or more moieties or conjugates which enhance the activity, cellular distribution or cellular uptake of the oligonucleotide. Such moieties 15 include but are not limited to lipid moieties such as a cholesterol moiety (Letsinger et al., *Proc. Natl. Acad. Sci. USA*, 1989, 86, 6553-6556), cholic acid (Manoharan et al., *Bioorg. Med. Chem. Lett.*, 1994, 4, 1053-1060), a thioether, e.g., hexyl-S-tritylthiol (Manoharan et al., *Ann. N.Y. Acad. Sci.*, 1992, 660, 306-309; Manoharan et al., *Bioorg. Med. Chem. Lett.*, 1993, 3, 2765-2770), a thiocholesterol (Oberhauser et al., *Nucl. Acids Res.*, 1992, 20, 533-538), an aliphatic chain, e.g., dodecandiol or undecyl 20 residues (Saison-Behmoaras et al., *EMBO J.*, 1991, 10, 1111-1118; Kabanov et al., *FEBS Lett.*, 1990, 259, 327-330; Svinarchuk et al., *Biochimie*, 1993, 75, 49-54), a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethylammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate (Manoharan et al., *Tetrahedron Lett.*, 1995, 36, 3651- 25 3654; Shea et al., *Nucl. Acids Res.*, 1990, 18, 3777-3783), a polyamine or a polyethylene glycol chain (Manoharan et al., *Nucleosides & Nucleotides*, 1995, 14, 969-973), or adamantan acetic acid (Manoharan et al., *Tetrahedron Lett.*, 1995, 36, 3651-3654), a palmityl moiety (Mishra et al., *Biochim. Biophys. Acta*, 1995, 1264, 229-237), or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety 30 (Crooke et al., *J. Pharmacol. Exp. Ther.*, 1996, 277, 923-937).

- 15 -

Representative United States patents that teach the preparation of such oligonucleotide conjugates include, but are not limited to, U.S. 4,828,979; 4,948,882; 5,218,105; 5,525,465; 5,541,313; 5,545,730; 5,552,538; 5,578,717, 5,580,731; 5,580,731; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486,603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025; 4,762,779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5,245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241, 5,391,723; 5,416,203, 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599,928 and 5,688,941, certain of which are commonly owned with the instant application, and each of which is herein incorporated by reference.

It is not necessary for all positions in a given compound to be uniformly modified, and in fact more than one of the aforementioned modifications may be incorporated in a single compound or even at a single nucleoside within an oligonucleotide. The present invention also includes antisense compounds which are chimeric compounds. "Chimeric" antisense compounds or "chimeras," in the context of this invention, are antisense compounds, particularly oligonucleotides, which contain two or more chemically distinct regions, each made up of at least one monomer unit, i.e., a nucleotide in the case of an oligonucleotide compound. These oligonucleotides typically contain at least one region wherein the oligonucleotide is modified so as to confer upon the oligonucleotide increased resistance to nuclease degradation, increased cellular uptake, and/or increased binding affinity for the target nucleic acid. An additional region of the oligonucleotide may serve as a substrate for enzymes capable of cleaving RNA:DNA or RNA:RNA hybrids. By way of example, RNase H is a cellular endonuclease which cleaves the RNA strand of an RNA:DNA duplex. Activation of RNase H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of oligonucleotide inhibition of gene expression. Consequently, comparable results can often be obtained with shorter oligonucleotides when chimeric oligonucleotides are used, compared to phosphorothioate deoxyoligonucleotides

- 16 -

hybridizing to the same target region. Cleavage of the RNA target can be routinely detected by gel electrophoresis and, if necessary, associated nucleic acid hybridization techniques known in the art.

Chimeric antisense compounds of the invention may be formed as composite structures of two or more oligonucleotides, modified oligonucleotides, oligonucleosides and/or oligonucleotide mimetics as described above. Such compounds have also been referred to in the art as hybrids or gapmers. Representative United States patents that teach the preparation of such hybrid structures include, but are not limited to, U.S.: 5,013,830; 5,149,797; 5,220,007; 5,256,775; 5,366,878; 5,403,711; 5,491,133; 5,565,350; 5,623,065; 5,652,355; 5,652,356; and 5,700,922, certain of which are commonly owned with the instant application, and each of which is herein incorporated by reference in its entirety.

The antisense compounds used in accordance with this invention may be conveniently and routinely made through the well-known technique of solid phase synthesis. Equipment for such synthesis is sold by several vendors including, for example, Applied Biosystems (Foster City, CA). Any other means for such synthesis known in the art may additionally or alternatively be employed. It is well known to use similar techniques to prepare oligonucleotides such as the phosphorothioates and alkylated derivatives.

The antisense compounds of the invention are synthesized *in vitro* and do not include antisense compositions of biological origin, or genetic vector constructs designed to direct the *in vivo* synthesis of antisense molecules.

The compounds of the invention may also be admixed, encapsulated, conjugated or otherwise associated with other molecules, molecule structures or mixtures of compounds, as for example, liposomes, receptor targeted molecules, oral, rectal, topical or other formulations, for assisting in uptake, distribution and/or absorption. Representative United States patents that teach the preparation of such uptake, distribution and/or absorption assisting formulations include, but are not limited to, U.S.: 5,108,921; 5,354,844; 5,416,016; 5,459,127; 5,521,291; 5,543,158; 5,547,932; 5,583,020; 5,591,721; 4,426,330; 4,534,899; 5,013,556; 5,108,921; 5,213,804;

- 17 -

5,227,170; 5,264,221; 5,356,633; 5,395,619; 5,416,016; 5,417,978; 5,462,854;
5,469,854; 5,512,295; 5,527,528; 5,534,259; 5,543,152; 5,556,948; 5,580,575; and
5,595,756, each of which is herein incorporated by reference.

The antisense compounds of the invention encompass any pharmaceutically acceptable salts, esters, or salts of such esters, or any other compound which, upon administration to an animal including a human, is capable of providing (directly or indirectly) the biologically active metabolite or residue thereof. Accordingly, for example, the disclosure is also drawn to prodrugs and pharmaceutically acceptable salts of the compounds of the invention, pharmaceutically acceptable salts of such prodrugs, and other bioequivalents.

The term "prodrug" indicates a therapeutic agent that is prepared in an inactive form that is converted to an active form (i.e., drug) within the body or cells thereof by the action of endogenous enzymes or other chemicals and/or conditions. In particular, prodrug versions of the oligonucleotides of the invention are prepared as SATE [(S-acetyl-2-thioethyl) phosphate] derivatives according to the methods disclosed in WO 93/24510 to Gosselin et al., published December 9, 1993 or in WO 94/26764 to Imbach et al.

The term "pharmaceutically acceptable salts" refers to physiologically and pharmaceutically acceptable salts of the compounds of the invention: i.e., salts that retain the desired biological activity of the parent compound and do not impart undesired toxicological effects thereto.

Pharmaceutically acceptable base addition salts are formed with metals or amines, such as alkali and alkaline earth metals or organic amines. Examples of metals used as cations are sodium, potassium, magnesium, calcium, and the like. Examples of suitable amines are N,N'-dibenzylethylenediamine, chloroprocaine, choline, diethanolamine, dicyclohexylamine, ethylenediamine, N-methylglucamine, and procaine (see, for example, Berge et al., "Pharmaceutical Salts," *J. of Pharma Sci.*, 1977, 66, 1-19). The base addition salts of said acidic compounds are prepared by contacting the free acid form with a sufficient amount of the desired base to produce the salt in the conventional manner. The free acid form may be regenerated by contacting the salt

- 18 -

form with an acid and isolating the free acid in the conventional manner. The free acid forms differ from their respective salt forms somewhat in certain physical properties such as solubility in polar solvents, but otherwise the salts are equivalent to their respective free acid for purposes of the present invention. As used herein, a

5 "pharmaceutical addition salt" includes a pharmaceutically acceptable salt of an acid form of one of the components of the compositions of the invention. These include organic or inorganic acid salts of the amines. Preferred acid salts are the hydrochlorides, acetates, salicylates, nitrates and phosphates. Other suitable pharmaceutically acceptable salts are well known to those skilled in the art and include

10 basic salts of a variety of inorganic and organic acids, such as, for example, with inorganic acids, such as for example hydrochloric acid, hydrobromic acid, sulfuric acid or phosphoric acid; with organic carboxylic, sulfonic, sulfo or phospho acids or N-substituted sulfamic acids, for example acetic acid, propionic acid, glycolic acid, succinic acid, maleic acid, hydroxymaleic acid, methylmaleic acid, fumaric acid, malic

15 acid, tartaric acid, lactic acid, oxalic acid, gluconic acid, glucaric acid, glucuronic acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, salicylic acid, 4-aminosalicylic acid, 2-phenoxybenzoic acid, 2-acetoxybenzoic acid, embonic acid, nicotinic acid or isonicotinic acid; and with amino acids, such as the 20 alpha-amino acids involved in the synthesis of proteins in nature, for example glutamic acid or aspartic acid, and also

20 with phenylacetic acid, methanesulfonic acid, ethanesulfonic acid, 2-hydroxyethanesulfonic acid, ethane-1,2-disulfonic acid, benzenesulfonic acid, 4-methylbenzenesulfoic acid, naphthalene-2-sulfonic acid, naphthalene-1,5-disulfonic acid, 2- or 3-phosphoglycerate, glucose-6-phosphate, N-cyclohexylsulfamic acid (with the formation of cyclamates), or with other acid organic compounds, such as ascorbic

25 acid. Pharmaceutically acceptable salts of compounds may also be prepared with a pharmaceutically acceptable cation. Suitable pharmaceutically acceptable cations are well known to those skilled in the art and include alkaline, alkaline earth, ammonium and quaternary ammonium cations. Carbonates or hydrogen carbonates are also possible.

- 19 -

For oligonucleotides, preferred examples of pharmaceutically acceptable salts include but are not limited to (a) salts formed with cations such as sodium, potassium, ammonium, magnesium, calcium, polyamines such as spermine and spermidine, etc.; (b) acid addition salts formed with inorganic acids, for example hydrochloric acid, 5 hydrobromic acid, sulfuric acid, phosphoric acid, nitric acid and the like; (c) salts formed with organic acids such as, for example, acetic acid, oxalic acid, tartaric acid, succinic acid, maleic acid, fumaric acid, gluconic acid, citric acid, malic acid, ascorbic acid, benzoic acid, tannic acid, palmitic acid, alginic acid, polyglutamic acid, naphthalenesulfonic acid, methanesulfonic acid, p-toluenesulfonic acid, 10 naphthalenedisulfonic acid, polygalacturonic acid, and the like; and (d) salts formed from elemental anions such as chlorine, bromine, and iodine.

The antisense compounds of the present invention can be utilized for diagnostics, therapeutics, prophylaxis and as research reagents and kits. For therapeutics, an animal, preferably a human, suspected of having a disease or disorder which can be treated by modulating the expression of PTP1B is treated by administering antisense 15 compounds in accordance with this invention. The compounds of the invention can be utilized in pharmaceutical compositions by adding an effective amount of an antisense compound to a suitable pharmaceutically acceptable diluent or carrier. Use of the antisense compounds and methods of the invention may also be useful prophylactically, 20 e.g., to prevent or delay infection, inflammation or tumor formation, for example.

The antisense compounds of the invention are useful for research and diagnostics, because these compounds hybridize to nucleic acids encoding PTP1B, enabling sandwich and other assays to easily be constructed to exploit this fact. Hybridization of the antisense oligonucleotides of the invention with a nucleic acid 25 encoding PTP1B can be detected by means known in the art. Such means may include conjugation of an enzyme to the oligonucleotide, radiolabelling of the oligonucleotide or any other suitable detection means. Kits using such detection means for detecting the level of PTP1B in a sample may also be prepared.

The present invention also includes pharmaceutical compositions and 30 formulations which include the antisense compounds of the invention. The

- 20 -

pharmaceutical compositions of the present invention may be administered in a number of ways depending upon whether local or systemic treatment is desired and upon the area to be treated. Administration may be topical (including ophthalmic and to mucous membranes including vaginal and rectal delivery), pulmonary, e.g., by inhalation or insufflation of powders or aerosols, including by nebulizer; intratracheal, intranasal, epidermal and transdermal), oral or parenteral. Parenteral administration includes intravenous, intraarterial, subcutaneous, intraperitoneal or intramuscular injection or infusion; or intracranial, e.g., intrathecal or intraventricular, administration.

Oligonucleotides with at least one 2'-O-methoxyethyl modification are believed to be particularly useful for oral administration.

Pharmaceutical compositions and formulations for topical administration may include transdermal patches, ointments, lotions, creams, gels, drops, suppositories, sprays, liquids and powders. Conventional pharmaceutical carriers, aqueous, powder or oily bases, thickeners and the like may be necessary or desirable. Coated condoms, gloves and the like may also be useful.

Compositions and formulations for oral administration include powders or granules, suspensions or solutions in water or non-aqueous media, capsules, sachets or tablets. Thickeners, flavoring agents, diluents, emulsifiers, dispersing aids or binders may be desirable.

Compositions and formulations for parenteral, intrathecal or intraventricular administration may include sterile aqueous solutions which may also contain buffers, diluents and other suitable additives such as, but not limited to, penetration enhancers, carrier compounds and other pharmaceutically acceptable carriers or excipients.

Pharmaceutical compositions of the present invention include, but are not limited to, solutions, emulsions, and liposome-containing formulations. These compositions may be generated from a variety of components that include, but are not limited to, preformed liquids, self-emulsifying solids and self-emulsifying semisolids.

The pharmaceutical formulations of the present invention, which may conveniently be presented in unit dosage form, may be prepared according to conventional techniques well known in the pharmaceutical industry. Such techniques

- 21 -

include the step of bringing into association the active ingredients with the pharmaceutical carrier(s) or excipient(s). In general the formulations are prepared by uniformly and intimately bringing into association the active ingredients with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product.

The compositions of the present invention may be formulated into any of many possible dosage forms such as, but not limited to, tablets, capsules, liquid syrups, soft gels, suppositories, and enemas. The compositions of the present invention may also be formulated as suspensions in aqueous, non-aqueous or mixed media. Aqueous suspensions may further contain substances which increase the viscosity of the suspension including, for example, sodium carboxymethylcellulose, sorbitol and/or dextran. The suspension may also contain stabilizers.

In one embodiment of the present invention the pharmaceutical compositions may be formulated and used as foams. Pharmaceutical foams include formulations such as, but not limited to, emulsions, microemulsions, creams, jellies and liposomes. While basically similar in nature these formulations vary in the components and the consistency of the final product. The preparation of such compositions and formulations is generally known to those skilled in the pharmaceutical and formulation arts and may be applied to the formulation of the compositions of the present invention.

20 Emulsions

The compositions of the present invention may be prepared and formulated as emulsions. Emulsions are typically heterogenous systems of one liquid dispersed in another in the form of droplets usually exceeding 0.1 μm in diameter. (Idson, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Bunker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199; Rosoff, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Bunker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., Volume 1, p. 245; Block in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Bunker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 2, p. 335; Higuchi *et al.*, in *Remington's Pharmaceutical Sciences*, Mack Publishing Co., Easton,

- 22 -

PA, 1985, p. 301). Emulsions are often biphasic systems comprising of two immiscible liquid phases intimately mixed and dispersed with each other. In general, emulsions may be either water-in-oil (w/o) or of the oil-in-water (o/w) variety. When an aqueous phase is finely divided into and dispersed as minute droplets into a bulk oily phase the resulting composition is called a water-in-oil (w/o) emulsion. Alternatively, when an oily phase is finely divided into and dispersed as minute droplets into a bulk aqueous phase the resulting composition is called an oil-in-water (o/w) emulsion. Emulsions may contain additional components in addition to the dispersed phases and the active drug which may be present as a solution in either the aqueous phase, oily phase or itself as a separate phase. Pharmaceutical excipients such as emulsifiers, stabilizers, dyes, and anti-oxidants may also be present in emulsions as needed. Pharmaceutical emulsions may also be multiple emulsions that are comprised of more than two phases such as, for example, in the case of oil-in-water-in-oil (o/w/o) and water-in-oil-in-water (w/o/w) emulsions. Such complex formulations often provide certain advantages that simple binary emulsions do not. Multiple emulsions in which individual oil droplets of an o/w emulsion enclose small water droplets constitute a w/o/w emulsion. Likewise a system of oil droplets enclosed in globules of water stabilized in an oily continuous provides an o/w/o emulsion.

Emulsions are characterized by little or no thermodynamic stability. Often, the dispersed or discontinuous phase of the emulsion is well dispersed into the external or continuous phase and maintained in this form through the means of emulsifiers or the viscosity of the formulation. Either of the phases of the emulsion may be a semisolid or a solid, as is the case of emulsion-style ointment bases and creams. Other means of stabilizing emulsions entail the use of emulsifiers that may be incorporated into either phase of the emulsion. Emulsifiers may broadly be classified into four categories: synthetic surfactants, naturally occurring emulsifiers, absorption bases, and finely dispersed solids (Idson, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199).

Synthetic surfactants, also known as surface active agents, have found wide applicability in the formulation of emulsions and have been reviewed in the literature

- 23 -

(Rieger, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 285; Idson, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), Marcel Dekker, Inc., New York, N.Y., 1988, volume 1, p. 199). Surfactants are typically amphiphilic and comprise a hydrophilic and a hydrophobic portion. The ratio of the hydrophilic to the hydrophobic nature of the surfactant has been termed the hydrophile/lipophile balance (HLB) and is a valuable tool in categorizing and selecting surfactants in the preparation of formulations. Surfactants may be classified into different classes based on the nature of the hydrophilic group: nonionic, anionic, cationic and amphoteric

5 (Rieger, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 10 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 285).

Naturally occurring emulsifiers used in emulsion formulations include lanolin, beeswax, phosphatides, lecithin and acacia. Absorption bases possess hydrophilic properties such that they can soak up water to form w/o emulsions yet retain their 15 semisolid consistencies, such as anhydrous lanolin and hydrophilic petrolatum. Finely divided solids have also been used as good emulsifiers especially in combination with surfactants and in viscous preparations. These include polar inorganic solids, such as heavy metal hydroxides, nonswelling clays such as bentonite, attapulgite, hectorite, kaolin, montmorillonite, colloidal aluminum silicate and colloidal magnesium aluminum 20 silicate, pigments and nonpolar solids such as carbon or glyceryl tristearate.

A large variety of non-emulsifying materials are also included in emulsion formulations and contribute to the properties of emulsions. These include fats, oils, waxes, fatty acids, fatty alcohols, fatty esters, humectants, hydrophilic colloids, preservatives and antioxidants (Block, in *Pharmaceutical Dosage Forms*, Lieberman, 25 Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 335; Idson, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199).

Hydrophilic colloids or hydrocolloids include naturally occurring gums and synthetic polymers such as polysaccharides (for example, acacia, agar, alginic acid, 30 carrageenan, guar gum, karaya gum, and tragacanth), cellulose derivatives (for

- 24 -

example, carboxymethylcellulose and carboxypropylcellulose), and synthetic polymers (for example, carbomers, cellulose ethers, and carboxyvinyl polymers). These disperse or swell in water to form colloidal solutions that stabilize emulsions by forming strong interfacial films around the dispersed-phase droplets and by increasing the viscosity of
5 the external phase.

Since emulsions often contain a number of ingredients such as carbohydrates, proteins, sterols and phosphatides that may readily support the growth of microbes, these formulations often incorporate preservatives. Commonly used preservatives included in emulsion formulations include methyl paraben, propyl paraben, quaternary 10 ammonium salts, benzalkonium chloride, esters of p-hydroxybenzoic acid, and boric acid. Antioxidants are also commonly added to emulsion formulations to prevent deterioration of the formulation. Antioxidants used may be free radical scavengers such as tocopherols, alkyl gallates, butylated hydroxyanisole, butylated hydroxytoluene, or reducing agents such as ascorbic acid and sodium metabisulfite, and antioxidant 15 synergists such as citric-acid, tartaric acid, and lecithin.

The application of emulsion formulations via dermatological, oral and parenteral routes and methods for their manufacture have been reviewed in the literature (Idson, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199). Emulsion formulations for oral 20 delivery have been very widely used because of reasons of ease of formulation, efficacy from an absorption and bioavailability standpoint. (Rosoff, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 245; Idson, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199).
25 Mineral-oil base laxatives, oil-soluble vitamins and high fat nutritive preparations are among the materials that have commonly been administered orally as o/w emulsions.

In one embodiment of the present invention, the compositions of oligonucleotides and nucleic acids are formulated as microemulsions. A microemulsion may be defined as a system of water, oil and amphiphile which is a single optically 30 isotropic and thermodynamically stable liquid solution (Rosoff, in *Pharmaceutical*

- 25 -

Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 245). Typically microemulsions are systems that are prepared by first dispersing an oil in an aqueous surfactant solution and then adding a sufficient amount of a fourth component, generally an intermediate chain-length alcohol 5 to form a transparent system. Therefore, microemulsions have also been described as thermodynamically stable, isotropically clear dispersions of two immiscible liquids that are stabilized by interfacial films of surface-active molecules (Leung and Shah, in: Controlled Release of Drugs: Polymers and Aggregate Systems, Rosoff, M., Ed., 1989, VCH Publishers, New York, pages 185-215). Microemulsions commonly are 10 prepared via a combination of three to five components that include oil, water, surfactant, cosurfactant and electrolyte. Whether the microemulsion is of the water-in-oil (w/o) or an oil-in-water (o/w) type is dependent on the properties of the oil and surfactant used and on the structure and geometric packing of the polar heads and hydrocarbon tails of the surfactant molecules (Schott, in Remington's Pharmaceutical Sciences, Mack Publishing Co., Easton, PA, 1985, p. 271).

The phenomenological approach utilizing phase diagrams has been extensively studied and has yielded a comprehensive knowledge, to one skilled in the art, of how to formulate microemulsions (Rosoff, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 245; Block, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 335). Compared to conventional emulsions, microemulsions offer the advantage of solubilizing water-insoluble drugs in a formulation of thermodynamically stable droplets that are formed spontaneously.

Surfactants used in the preparation of microemulsions include, but are not limited to, ionic surfactants, non-ionic surfactants, Brij 96, polyoxyethylene oleyl ethers, polyglycerol fatty acid esters, tetraglycerol monolaurate (ML310), tetraglycerol monooleate (MO310), hexaglycerol monooleate (PO310), hexaglycerol pentaoleate (PO500), decaglycerol monocaprate (MCA750), decaglycerol monooleate (MO750), 25 decaglycerol sequioleate (SO750), decaglycerol deaoleate (DAO750), alone or in 30

- 26 -

combination with cosurfactants. The cosurfactant, usually a short-chain alcohol such as ethanol, 1-propanol, and 1-butanol, serves to increase the interfacial fluidity by penetrating into the surfactant film and consequently creating a disordered film because of the void space generated among surfactant molecules. Microemulsions may, 5 however, be prepared without the use of cosurfactants and alcohol-free self-emulsifying microemulsion systems are known in the art. The aqueous phase may typically be, but is not limited to, water, an aqueous solution of the drug, glycerol, PEG300, PEG400, polyglycerols, propylene glycols, and derivatives of ethylene glycol. The oil phase may include, but is not limited to, materials such as Captex 300, Captex 355, Capmul MCM, 10 fatty acid esters, medium chain (C8-C12) mono, di, and tri-glycerides, polyoxyethylated glyceryl fatty acid esters, fatty alcohols, polyglycolized glycerides, saturated polyglycolized C8-C10 glycerides, vegetable oils and silicone oil.

Microemulsions are particularly of interest from the standpoint of drug solubilization and the enhanced absorption of drugs. Lipid based microemulsions (both 15 o/w and w/o) have been proposed to enhance the oral bioavailability of drugs, including peptides (Constantinides et al., *Pharmaceutical Research*, 1994, 11, 1385-1390; Ritschel, *Meth. Find. Exp. Clin. Pharmacol.*, 1993, 13, 205). Microemulsions afford advantages of improved drug solubilization, protection of drug from enzymatic hydrolysis, possible enhancement of drug absorption due to surfactant-induced 20 alterations in membrane fluidity and permeability, ease of preparation, ease of oral administration over solid dosage forms, improved clinical potency, and decreased toxicity (Constantinides et al., *Pharmaceutical Research*, 1994, 11, 1385; Ho et al., *J. Pharm. Sci.*, 1996, 85, 138-143). Often microemulsions may form spontaneously when their components are brought together at ambient temperature. This may be 25 particularly advantageous when formulating thermolabile drugs, peptides or oligonucleotides. Microemulsions have also been effective in the transdermal delivery of active components in both cosmetic and pharmaceutical applications. It is expected that the microemulsion compositions and formulations of the present invention will facilitate the increased systemic absorption of oligonucleotides and nucleic acids from 30 the gastrointestinal tract, as well as improve the local cellular uptake of

- 27 -

oligonucleotides and nucleic acids within the gastrointestinal tract, vagina, buccal cavity and other areas of administration.

Microemulsions of the present invention may also contain additional components and additives such as sorbitan monostearate (Grill 3), Labrasol, and penetration enhancers to improve the properties of the formulation and to enhance the absorption of the oligonucleotides and nucleic acids of the present invention. Penetration enhancers used in the microemulsions of the present invention may be classified as belonging to one of five broad categories - surfactants, fatty acids, bile salts, chelating agents, and non-chelating non-surfactants (Lee *et al.*, *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, p. 92). Each of these classes has been discussed above.

Liposomes

There are many organized surfactant structures besides microemulsions that have been studied and used for the formulation of drugs. These include monolayers, micelles, bilayers and vesicles. Vesicles, such as liposomes, have attracted great interest because of their specificity and the duration of action they offer from the standpoint of drug delivery. As used in the present invention, the term "liposome" means a vesicle composed of amphiphilic lipids arranged in a spherical bilayer or bilayers.

Liposomes are unilamellar or multilamellar vesicles which have a membrane formed from a lipophilic material and an aqueous interior. The aqueous portion contains the composition to be delivered. Cationic liposomes possess the advantage of being able to fuse to the cell wall. Non-cationic liposomes, although not able to fuse as efficiently with the cell wall, are taken up by macrophages *in vivo*.

In order to cross intact mammalian skin, lipid vesicles must pass through a series of fine pores, each with a diameter less than 50 nm, under the influence of a suitable transdermal gradient. Therefore, it is desirable to use a liposome which is highly deformable and able to pass through such fine pores.

Further advantages of liposomes include; liposomes obtained from natural phospholipids are biocompatible and biodegradable; liposomes can incorporate a wide

- 28 -

range of water and lipid soluble drugs; liposomes can protect encapsulated drugs in their internal compartments from metabolism and degradation (Rosoff, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Bunker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 245). Important considerations in the preparation of liposome formulations are the lipid surface charge, vesicle size and the aqueous volume of the liposomes.

Liposomes are useful for the transfer and delivery of active ingredients to the site of action. Because the liposomal membrane is structurally similar to biological membranes, when liposomes are applied to a tissue, the liposomes start to merge with the cellular membranes. As the merging of the liposome and cell progresses, the 10 liposomal contents are emptied into the cell where the active agent may act.

Liposomal formulations have been the focus of extensive investigation as the mode of delivery for many drugs. There is growing evidence that for topical administration, liposomes present several advantages over other formulations. Such 15 advantages include reduced side-effects related to high systemic absorption of the administered drug, increased accumulation of the administered drug at the desired target, and the ability to administer a wide variety of drugs, both hydrophilic and hydrophobic, into the skin.

Several reports have detailed the ability of liposomes to deliver agents including 20 high-molecular weight DNA into the skin. Compounds including analgesics, antibodies, hormones and high-molecular weight DNAs have been administered to the skin. The majority of applications resulted in the targeting of the upper epidermis.

Liposomes fall into two broad classes. Cationic liposomes are positively charged 25 liposomes which interact with the negatively charged DNA molecules to form a stable complex. The positively charged DNA/liposome complex binds to the negatively charged cell surface and is internalized in an endosome. Due to the acidic pH within the endosome, the liposomes are ruptured, releasing their contents into the cell cytoplasm (Wang *et al.*, *Biochem. Biophys. Res. Commun.*, 1987, 147, 980-985).

Liposomes which are pH-sensitive or negatively-charged, entrap DNA rather 30 than complex with it. Since both the DNA and the lipid are similarly charged, repulsion

- 29 -

rather than complex formation occurs. Nevertheless, some DNA is entrapped within the aqueous interior of these liposomes. pH-sensitive liposomes have been used to deliver DNA encoding the thymidine kinase gene to cell monolayers in culture. Expression of the exogenous gene was detected in the target cells (*Zhou et al., Journal of Controlled Release, 1992, 19, 269-274*).

One major type of liposomal composition includes phospholipids other than naturally-derived phosphatidylcholine. Neutral liposome compositions, for example, can be formed from dimyristoyl phosphatidylcholine (DMPC) or dipalmitoyl phosphatidylcholine (DPPC). Anionic liposome compositions generally are formed from dimyristoyl phosphatidylglycerol, while anionic fusogenic liposomes are formed primarily from dioleoyl phosphatidylethanolamine (DOPE). Another type of liposomal composition is formed from phosphatidylcholine (PC) such as, for example, soybean PC, and egg PC. Another type is formed from mixtures of phospholipid and/or phosphatidylcholine and/or cholesterol.

Several studies have assessed the topical delivery of liposomal drug formulations to the skin. Application of liposomes containing interferon to guinea pig skin resulted in a reduction of skin herpes sores while delivery of interferon via other means (e.g. as a solution or as an emulsion) were ineffective (*Weiner et al., Journal of Drug Targeting, 1992, 2, 405-410*). Further, an additional study tested the efficacy of interferon administered as part of a liposomal formulation to the administration of interferon using an aqueous system, and concluded that the liposomal formulation was superior to aqueous administration (*du Plessis et al., Antiviral Research, 1992, 18, 259-265*).

Non-ionic liposomal systems have also been examined to determine their utility in the delivery of drugs to the skin, in particular systems comprising non-ionic surfactant and cholesterol. Non-ionic liposomal formulations comprising Novasome™ I (glyceryl dilaurate/cholesterol/polyoxyethylene-10-stearyl ether) and Novasome™ II (glyceryl distearate/ cholesterol/polyoxyethylene-10-stearyl ether) were used to deliver cyclosporin-A into the dermis of mouse skin. Results indicated that such non-ionic

- 30 -

liposomal systems were effective in facilitating the deposition of cyclosporin-A into different layers of the skin (Hu et al. *S.T.P.Pharma. Sci.*, 1994, 4, 6, 466).

Liposomes also include "sterically stabilized" liposomes, a term which, as used herein, refers to liposomes comprising one or more specialized lipids that, when incorporated into liposomes, result in enhanced circulation lifetimes relative to liposomes lacking such specialized lipids. Examples of sterically stabilized liposomes are those in which part of the vesicle-forming lipid portion of the liposome (A) comprises one or more glycolipids, such as monosialoganglioside G_{M1}, or (B) is derivatized with one or more hydrophilic polymers, such as a polyethylene glycol (PEG) moiety. While not wishing to be bound by any particular theory, it is thought in the art that, at least for sterically stabilized liposomes containing gangliosides, sphingomyelin, or PEG-derivatized lipids, the enhanced circulation half-life of these sterically stabilized liposomes derives from a reduced uptake into cells of the reticuloendothelial system (RES) (Allen et al., *FEBS Letters*, 1987, 223, 42; Wu et al., *Cancer Research*, 1993, 53, 3765).

Various liposomes comprising one or more glycolipids are known in the art. Papahadjopoulos et al. (*Ann. N.Y. Acad. Sci.*, 1987, 507, 64) reported the ability of monosialoganglioside G_{M1}, galactocerebroside sulfate and phosphatidylinositol to improve blood half-lives of liposomes. These findings were expounded upon by Gabizon et al. (*Proc. Natl. Acad. Sci. U.S.A.*, 1988, 85, 6949). U.S. Patent No. 4,837,028 and WO 88/04924, both to Allen et al., disclose liposomes comprising (1) sphingomyelin and (2) the ganglioside G_{M1} or a galactocerebroside sulfate ester. U.S. Patent No. 5,543,152 (Webb et al.) discloses liposomes comprising sphingomyelin. Liposomes comprising 1,2-sn-dimyristoylphosphatidylcholine are disclosed in WO 97/13499 (Lim et al.).

Many liposomes comprising lipids derivatized with one or more hydrophilic polymers, and methods of preparation thereof, are known in the art. Sunamoto et al. (*Bull. Chem. Soc. Jpn.*, 1980, 53, 2778) described liposomes comprising a nonionic detergent, 2C₁₂15G, that contains a PEG moiety. Illum et al. (*FEBS Lett.*, 1984, 167, 79) noted that hydrophilic coating of polystyrene particles with polymeric glycals

results in significantly enhanced blood half-lives. Synthetic phospholipids modified by the attachment of carboxylic groups of polyalkylene glycols (e.g., PEG) are described by Sears (U.S. Patent Nos. 4,426,330 and 4,534,899). Klibanov *et al.* (*FEBS Lett.*, 1990, 268, 235) described experiments demonstrating that liposomes comprising phosphatidylethanolamine (PE) derivatized with PEG or PEG stearate have significant increases in blood circulation half-lives. Blume *et al.* (*Biochimica et Biophysica Acta*, 1990, 1029, 91) extended such observations to other PEG-derivatized phospholipids, e.g., DSPE-PEG, formed from the combination of distearoylphosphatidylethanolamine (DSPE) and PEG. Liposomes having covalently bound PEG moieties on their external surface are described in European Patent No. EP 0 445 131 B1 and WO 90/04384 to Fisher. Liposome compositions containing 1-20 mole percent of PE derivatized with PEG, and methods of use thereof, are described by Woodle *et al.* (U.S. Patent Nos. 5,013,556 and 5,356,633) and Martin *et al.* (U.S. Patent No. 5,213,804 and European Patent No. EP 0 496 813 B1). Liposomes comprising a number of other lipid-polymer conjugates are disclosed in WO 91/05545 and U.S. Patent No. 5,225,212 (both to Martin *et al.*) and in WO 94/20073 (Zalipsky *et al.*) Liposomes comprising PEG-modified ceramide lipids are described in WO 96/10391 (Choi *et al.*). U.S. Patent Nos. 5,540,935 (Miyazaki *et al.*) and 5,556,948 (Tagawa *et al.*) describe PEG-containing liposomes that can be further derivatized with functional moieties on their surfaces.

A limited number of liposomes comprising nucleic acids are known in the art. WO 96/40062 to Thierry *et al.* discloses methods for encapsulating high molecular weight nucleic acids in liposomes. U.S. Patent No. 5,264,221 to Tagawa *et al.* discloses protein-bonded liposomes and asserts that the contents of such liposomes may include an antisense RNA. U.S. Patent No. 5,665,710 to Rahman *et al.* describes certain methods of encapsulating oligodeoxynucleotides in liposomes. WO 97/04787 to Love *et al.* discloses liposomes comprising antisense oligonucleotides targeted to the raf gene.

Transfersomes are yet another type of liposomes, and are highly deformable lipid aggregates which are attractive candidates for drug delivery vehicles. Transfersomes may be described as lipid droplets which are so highly deformable that they are easily

- 32 -

able to penetrate through pores which are smaller than the droplet. Transfersomes are adaptable to the environment in which they are used, e.g. they are self-optimizing (adaptive to the shape of pores in the skin), self-repairing, frequently reach their targets without fragmenting, and often self-loading. To make transfersomes it is possible to
5 add surface edge-activators, usually surfactants, to a standard liposomal composition. Transfersomes have been used to deliver serum albumin to the skin. The transfersome-mediated delivery of serum albumin has been shown to be as effective as subcutaneous injection of a solution containing serum albumin.

Surfactants find wide application in formulations such as emulsions (including
10 microemulsions) and liposomes. The most common way of classifying and ranking the properties of the many different types of surfactants, both natural and synthetic, is by the use of the hydrophile/lipophile balance (HLB). The nature of the hydrophilic group (also known as the "head") provides the most useful means for categorizing the different surfactants used in formulations (Rieger, in *Pharmaceutical Dosage Forms*,
15 Marcel Dekker, Inc., New York, NY, 1988, p. 285).

If the surfactant molecule is not ionized, it is classified as a nonionic surfactant. Nonionic surfactants find wide application in pharmaceutical and cosmetic products and are usable over a wide range of pH values. In general their HLB values range from 2 to about 18 depending on their structure. Nonionic surfactants include nonionic esters
20 such as ethylene glycol esters, propylene glycol esters, glyceryl esters, polyglyceryl esters, sorbitan esters, sucrose esters, and ethoxylated esters. Nonionic alkanolamides and ethers such as fatty alcohol ethoxylates, propoxylated alcohols, and
25 ethoxylated/propoxylated block polymers are also included in this class. The polyoxyethylene surfactants are the most popular members of the nonionic surfactant class.

If the surfactant molecule carries a negative charge when it is dissolved or dispersed in water, the surfactant is classified as anionic. Anionic surfactants include carboxylates such as soaps, acyl lactylates, acyl amides of amino acids, esters of sulfuric acid such as alkyl sulfates and ethoxylated alkyl sulfates, sulfonates such as alkyl
30 benzene sulfonates, acyl isethionates, acyl taurates and sulfosuccinates, and phosphates.

- 33 -

The most important members of the anionic surfactant class are the alkyl sulfates and the soaps.

If the surfactant molecule carries a positive charge when it is dissolved or dispersed in water, the surfactant is classified as cationic. Cationic surfactants include 5 quaternary ammonium salts and ethoxylated amines. The quaternary ammonium salts are the most used members of this class.

If the surfactant molecule has the ability to carry either a positive or negative charge, the surfactant is classified as amphoteric. Amphoteric surfactants include acrylic acid derivatives, substituted alkylamides, N-alkylbetaines and phosphatides.

10 The use of surfactants in drug products, formulations and in emulsions has been reviewed (Rieger, in *Pharmaceutical Dosage Forms*, Marcel Dekker, Inc., New York, NY, 1988, p. 285).

Penetration Enhancers

In one embodiment, the present invention employs various penetration enhancers 15 to effect the efficient delivery of nucleic acids, particularly oligonucleotides, to the skin of animals. Most drugs are present in solution in both ionized and nonionized forms. However, usually only lipid soluble or lipophilic drugs readily cross cell membranes. It has been discovered that even non-lipophilic drugs may cross cell membranes if the membrane to be crossed is treated with a penetration enhancer. In addition to aiding 20 the diffusion of non-lipophilic drugs across cell membranes, penetration enhancers also enhance the permeability of lipophilic drugs.

Penetration enhancers may be classified as belonging to one of five broad categories, i.e., surfactants, fatty acids, bile salts, chelating agents, and non-chelating non-surfactants (Lee *et al.*, *Critical Reviews in Therapeutic Drug Carrier Systems*, 25 1991, p.92). Each of the above mentioned classes of penetration enhancers are described below in greater detail.

Surfactants: In connection with the present invention, surfactants (or "surface-active agents") are chemical entities which, when dissolved in an aqueous solution, reduce the surface tension of the solution or the interfacial tension between the aqueous

- 35 -

5 *Reviews in Therapeutic Drug Carrier Systems*, 1991, page 92; Swinyard, Chapter 39
In: *Remington's Pharmaceutical Sciences*, 18th Ed., Gennaro, ed., Mack Publishing
Co., Easton, PA, 1990, pages 782-783; Muranishi, *Critical Reviews in Therapeutic
Drug Carrier Systems*, 1990, 7, 1-33; Yamamoto *et al.*, *J. Pharm. Exp. Ther.*, 1992,
263, 25; Yamashita *et al.*, *J. Pharm. Sci.*, 1990, 79, 579-583).

10 Chelating Agents: Chelating agents, as used in connection with the present invention, can be defined as compounds that remove metallic ions from solution by forming complexes therewith, with the result that absorption of oligonucleotides through the mucosa is enhanced. With regards to their use as penetration enhancers in the present invention, chelating agents have the added advantage of also serving as DNase inhibitors, as most characterized DNA nucleases require a divalent metal ion for catalysis and are thus inhibited by chelating agents (Jarrett, *J. Chromatogr.*, 1993, 618, 315-339). Chelating agents of the invention include but are not limited to disodium ethylenediaminetetraacetate (EDTA), citric acid, salicylates (e.g., sodium salicylate, 5-methoxysalicylate and homovanilate), N-acyl derivatives of collagen, laureth-9 and N-amino acyl derivatives of beta-diketones (enamines) (Lee *et al.*, *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, page 92; Muranishi, *Critical Reviews in Therapeutic Drug Carrier Systems*, 1990, 7, 1-33; Buur *et al.*, *J. Control Rel.*, 1990, 14, 43-51).

20 Non-chelating non-surfactants: As used herein, non-chelating non-surfactant penetration enhancing compounds can be defined as compounds that demonstrate insignificant activity as chelating agents or as surfactants but that nonetheless enhance absorption of oligonucleotides through the alimentary mucosa (Muranishi, *Critical Reviews in Therapeutic Drug Carrier Systems*, 1990, 7, 1-33). This class of penetration enhancers include, for example, unsaturated cyclic ureas, 1-alkyl- and 1-alkenylazacyclo-alkanone derivatives (Lee *et al.*, *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, page 92); and non-steroidal anti-inflammatory agents such as diclofenac sodium, indomethacin and phenylbutazone (Yamashita *et al.*, *J. Pharm. Pharmacol.*, 1987, 39, 621-626).

- 36 -

Agents that enhance uptake of oligonucleotides at the cellular level may also be added to the pharmaceutical and other compositions of the present invention. For example, cationic lipids, such as lipofectin (Junichi *et al.*, U.S. Patent No. 5,705,188), cationic glycerol derivatives, and polycationic molecules, such as polylysine (Lollo *et al.*, PCT Application WO 97/30731), are also known to enhance the cellular uptake of oligonucleotides.

Other agents may be utilized to enhance the penetration of the administered nucleic acids, including glycols such as ethylene glycol and propylene glycol, pyrrols such as 2-pyrrol, azones, and terpenes such as limonene and menthone.

10 Carriers

Certain compositions of the present invention also incorporate carrier compounds in the formulation. As used herein, "carrier compound" or "carrier" can refer to a nucleic acid, or analog thereof, which is inert (*i.e.*, does not possess biological activity *per se*) but is recognized as a nucleic acid by *in vivo* processes that reduce the 15 bioavailability of a nucleic acid having biological activity by, for example, degrading the biologically active nucleic acid or promoting its removal from circulation. The coadministration of a nucleic acid and a carrier compound, typically with an excess of the latter substance, can result in a substantial reduction of the amount of nucleic acid recovered in the liver, kidney or other extracirculatory reservoirs, presumably due to 20 competition between the carrier compound and the nucleic acid for a common receptor. For example, the recovery of a partially phosphorothioate oligonucleotide in hepatic tissue can be reduced when it is coadministered with polyinosinic acid, dextran sulfate, polycytidic acid or 4-acetamido-4'isothiocyanostilbene-2,2'-disulfonic acid (Miyao *et al.*, *Antisense Res. Dev.*, 1995, 5, 115-121; Takakura *et al.*, *Antisense & Nucl. Acid Drug Dev.*, 1996, 6, 177-183).

Excipients

In contrast to a carrier compound, a "pharmaceutical carrier" or "excipient" is a pharmaceutically acceptable solvent, suspending agent or any other pharmacologically

- 37 -

inert vehicle for delivering one or more nucleic acids to an animal. The excipient may be liquid or solid and is selected, with the planned manner of administration in mind, so as to provide for the desired bulk, consistency, *etc.*, when combined with a nucleic acid and the other components of a given pharmaceutical composition. Typical
5 pharmaceutical carriers include, but are not limited to, binding agents (*e.g.*, pregelatinized maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose, *etc.*); fillers (*e.g.*, lactose and other sugars, microcrystalline cellulose, pectin, gelatin, calcium sulfate, ethyl cellulose, polyacrylates or calcium hydrogen phosphate, *etc.*); lubricants (*e.g.*, magnesium stearate, talc, silica, colloidal silicon dioxide, stearic acid,
10 metallic stearates, hydrogenated vegetable oils, corn starch, polyethylene glycols, sodium benzoate, sodium acetate, *etc.*); disintegrants (*e.g.*, starch, sodium starch glycolate, *etc.*); and wetting agents (*e.g.*, sodium lauryl sulphate, *etc.*).

Pharmaceutically acceptable organic or inorganic excipient suitable for non-parenteral administration which do not deleteriously react with nucleic acids can also be
15 used to formulate the compositions of the present invention. Suitable pharmaceutically acceptable carriers include, but are not limited to, water, salt solutions, alcohols, polyethylene glycols, gelatin, lactose, amylose, magnesium stearate, talc, silicic acid, viscous paraffin, hydroxymethylcellulose, polyvinylpyrrolidone and the like.

Formulations for topical administration of nucleic acids may include sterile and
20 non-sterile aqueous solutions, non-aqueous solutions in common solvents such as alcohols, or solutions of the nucleic acids in liquid or solid oil bases. The solutions may also contain buffers, diluents and other suitable additives. Pharmaceutically acceptable organic or inorganic excipients suitable for non-parenteral administration which do not deleteriously react with nucleic acids can be used.

25 Suitable pharmaceutically acceptable excipients include, but are not limited to, water, salt solutions, alcohol, polyethylene glycols, gelatin, lactose, amylose, magnesium stearate, talc, silicic acid, viscous paraffin, hydroxymethylcellulose, polyvinylpyrrolidone and the like.

- 39 -

ganciclovir, may also be combined in compositions of the invention. See, generally, *The Merck Manual of Diagnosis and Therapy*, 15th Ed., Berkow et al., eds., 1987, Rahway, N.J., pages 2499-2506 and 46-49, respectively). Other non-antisense chemotherapeutic agents are also within the scope of this invention. Two or more 5 combined compounds may be used together or sequentially.

In another related embodiment, compositions of the invention may contain one or more antisense compounds, particularly oligonucleotides, targeted to a first nucleic acid and one or more additional antisense compounds targeted to a second nucleic acid target. Numerous examples of antisense compounds are known in the art. Two or more 10 combined compounds may be used together or sequentially.

The formulation of therapeutic compositions and their subsequent administration is believed to be within the skill of those in the art. Dosing is dependent on severity and responsiveness of the disease state to be treated, with the course of treatment lasting from several days to several months, or until a cure is effected or a diminution of the 15 disease state is achieved. Optimal dosing schedules can be calculated from measurements of drug accumulation in the body of the patient. Persons of ordinary skill can easily determine optimum dosages, dosing methodologies and repetition rates. Optimum dosages may vary depending on the relative potency of individual oligonucleotides, and can generally be estimated based on EC₅₀s found to be effective in 20 in vitro and in vivo animal models. In general, dosage is from 0.01 ug to 100 g per kg of body weight, and may be given once or more daily, weekly, monthly or yearly, or even once every 2 to 20 years. Persons of ordinary skill in the art can easily estimate repetition rates for dosing based on measured residence times and concentrations of the drug in bodily fluids or tissues. Following successful treatment, it may be desirable to 25 have the patient undergo maintenance therapy to prevent the recurrence of the disease state, wherein the oligonucleotide is administered in maintenance doses, ranging from 0.01 ug to 100 g per kg of body weight, once or more daily, to once every 20 years.

While the present invention has been described with specificity in accordance with certain of its preferred embodiments, the following examples serve only to 30 illustrate the invention and are not intended to limit the same.

- 40 -

EXAMPLES

Example 1

Nucleoside Phosphoramidites for Oligonucleotide Synthesis

Deoxy and 2'-alkoxy amidites

5 2'-Deoxy and 2'-methoxy beta-cyanoethylisopropyl phosphoramidites were purchased from commercial sources (e.g. Chemgenes, Needham MA or Glen Research, Inc. Sterling VA). Other 2'-O-alkoxy substituted nucleoside amidites are prepared as described in U.S. Patent 5,506,351, herein incorporated by reference. For oligonucleotides synthesized using 2'-alkoxy amidites, the standard cycle for
10 unmodified oligonucleotides was utilized, except the wait step after pulse delivery of tetrazole and base was increased to 360 seconds.

15 Oligonucleotides containing 5-methyl-2'-deoxycytidine (5-Me-C) nucleotides were synthesized according to published methods [Sanghvi, et. al., *Nucleic Acids Research*, 1993, 21, 3197-3203] using commercially available phosphoramidites (Glen Research, Sterling VA or ChemGenes, Needham MA).

2'-Fluoro amidites

2'-Fluorodeoxyadenosine amidites

20 2'-fluoro oligonucleotides were synthesized as described previously [Kawasaki, et. al., *J. Med. Chem.*, 1993, 36, 831-841] and United States patent 5,670,633, herein incorporated by reference. Briefly, the protected nucleoside N6-benzoyl-2'-deoxy-2'-fluoroadenosine was synthesized utilizing commercially available 9-beta-D-arabinofuranosyladenine as starting material and by modifying literature procedures whereby the 2'-alpha-fluoro atom is introduced by a S_N2-displacement of a 2'-beta-trityl group. Thus N6-benzoyl-9-beta-D-arabinofuranosyladenine was selectively protected in moderate yield as the 3',5'-ditetrahydropyranyl (THP) intermediate.
25 Deprotection of the THP and N6-benzoyl groups was accomplished using standard methodologies and standard methods were used to obtain the 5'-dimethoxytrityl-(DMT) and 5'-DMT-3'-phosphoramidite intermediates.

- 41 -

2'-Fluorodeoxyguanosine

The synthesis of 2'-deoxy-2'-fluoroguanosine was accomplished using tetraisopropylsiloxanyl (TPDS) protected 9-beta-D-arabinofuranosylguanine as starting material, and conversion to the intermediate diisobutryl-
5 arabinofuranosylguanosine. Deprotection of the TPDS group was followed by protection of the hydroxyl group with THP to give diisobutryl di-THP protected arabinofuranosylguanine. Selective O-deacylation and triflation was followed by treatment of the crude product with fluoride, then deprotection of the THP groups. Standard methodologies were used to obtain the 5'-DMT- and 5'-DMT-3'-
10 phosphoramidites.

2'-Fluorouridine

Synthesis of 2'-deoxy-2'-fluorouridine was accomplished by the modification of a literature procedure in which 2,2'-anhydro-1-beta-D-arabinofuranosyluracil was treated with 70% hydrogen fluoride-pyridine. Standard procedures were used to obtain
15 the 5'-DMT and 5'-DMT-3'phosphoramidites.

2'-Fluorodeoxycytidine

2'-deoxy-2'-fluorocytidine was synthesized via amination of 2'-deoxy-2'-fluorouridine, followed by selective protection to give N4-benzoyl-2'-deoxy-2'-fluorocytidine. Standard procedures were used to obtain the 5'-DMT and 5'-DMT-
20 3'phosphoramidites.

2'-O-(2-Methoxyethyl) modified amidites

2'-O-Methoxyethyl-substituted nucleoside amidites are prepared as follows, or alternatively, as per the methods of Martin, P., *Helvetica Chimica Acta*, 1995, 78, 486-504.

- 42 -

2,2'-Anhydro[1-(beta-D-arabinofuranosyl)-5-methyluridine]

5-Methyluridine (ribosylthymine, commercially available through Yamasa, Choshi, Japan) (72.0 g, 0.279 M), diphenylcarbonate (90.0 g, 0.420 M) and sodium bicarbonate (2.0 g, 0.024 M) were added to DMF (300 mL). The mixture was heated to reflux, with stirring, allowing the evolved carbon dioxide gas to be released in a controlled manner. After 1 hour, the slightly darkened solution was concentrated under reduced pressure. The resulting syrup was poured into diethylether (2.5 L), with stirring. The product formed a gum. The ether was decanted and the residue was dissolved in a minimum amount of methanol (ca. 400 mL). The solution was poured into fresh ether (2.5 L) to yield a stiff gum. The ether was decanted and the gum was dried in a vacuum oven (60°C at 1 mm Hg for 24 h) to give a solid that was crushed to a light tan powder (57 g, 85% crude yield). The NMR spectrum was consistent with the structure, contaminated with phenol as its sodium salt (ca. 5%). The material was used as is for further reactions (or it can be purified further by column chromatography using a gradient of methanol in ethyl acetate (10-25%) to give a white solid, mp 222-4°C).

2'-O-Methoxyethyl-5-methyluridine

2,2'-Anhydro-5-methyluridine (195 g, 0.81 M), tris(2-methoxyethyl)borate (231 g, 0.98 M) and 2-methoxyethanol (1.2 L) were added to a 2 L stainless steel pressure vessel and placed in a pre-heated oil bath at 160°C. After heating for 48 hours at 155-160°C, the vessel was opened and the solution evaporated to dryness and triturated with MeOH (200 mL). The residue was suspended in hot acetone (1 L). The insoluble salts were filtered, washed with acetone (150 mL) and the filtrate evaporated. The residue (280 g) was dissolved in CH₃CN (600 mL) and evaporated. A silica gel column (3 kg) was packed in CH₂Cl₂/acetone/MeOH (20:5:3) containing 0.5% Et₃NH. The residue was dissolved in CH₂Cl₂ (250 mL) and adsorbed onto silica (150 g) prior to loading onto the column. The product was eluted with the packing solvent to give 160 g (63%) of product. Additional material was obtained by reworking impure fractions.

- 43 -

2'-O-Methoxyethyl-5'-O-dimethoxytrityl-5-methyluridine

2'-O-Methoxyethyl-5-methyluridine (160 g, 0.506 M) was co-evaporated with pyridine (250 mL) and the dried residue dissolved in pyridine (1.3 L). A first aliquot of dimethoxytrityl chloride (94.3 g, 0.278 M) was added and the mixture stirred at room 5 temperature for one hour. A second aliquot of dimethoxytrityl chloride (94.3 g, 0.278 M) was added and the reaction stirred for an additional one hour. Methanol (170 mL) was then added to stop the reaction. HPLC showed the presence of approximately 70% product. The solvent was evaporated and triturated with CH₃CN (200 mL). The residue was dissolved in CHCl₃ (1.5 L) and extracted with 2x500 mL of saturated 10 NaHCO₃ and 2x500 mL of saturated NaCl. The organic phase was dried over Na₂SO₄, filtered and evaporated. 275 g of residue was obtained. The residue was purified on a 3.5 kg silica gel column, packed and eluted with EtOAc/hexane/acetone (5:5:1) containing 0.5% Et₃NH. The pure fractions were evaporated to give 164 g of product. Approximately 20 g additional was obtained from the impure fractions to give a total 15 yield of 183 g (57%).

3'-O-Acetyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyluridine

2'-O-Methoxyethyl-5'-O-dimethoxytrityl-5-methyluridine (106 g, 0.167 M), DMF/pyridine (750 mL of a 3:1 mixture prepared from 562 mL of DMF and 188 mL of pyridine) and acetic anhydride (24.38 mL, 0.258 M) were combined and stirred at room 20 temperature for 24 hours. The reaction was monitored by TLC by first quenching the TLC sample with the addition of MeOH. Upon completion of the reaction, as judged by TLC, MeOH (50 mL) was added and the mixture evaporated at 35 °C. The residue was dissolved in CHCl₃ (800 mL) and extracted with 2x200 mL of saturated sodium bicarbonate and 2x200 mL of saturated NaCl. The water layers were back extracted 25 with 200 mL of CHCl₃. The combined organics were dried with sodium sulfate and evaporated to give 122 g of residue (approx. 90% product). The residue was purified on a 3.5 kg silica gel column and eluted using EtOAc/hexane(4:1). Pure product fractions were evaporated to yield 96 g (84%). An additional 1.5 g was recovered from later fractions.

- 44 -

3'-O-Acetyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyl-4-triazoleuridine

A first solution was prepared by dissolving 3'-O-acetyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyluridine (96 g, 0.144 M) in CH₃CN (700 mL) and set aside.

5 Triethylamine (189 mL, 1.44 M) was added to a solution of triazole (90 g, 1.3 M) in CH₃CN (1 L), cooled to -5°C and stirred for 0.5 h using an overhead stirrer. POCl₃ was added dropwise, over a 30 minute period, to the stirred solution maintained at 0-10°C, and the resulting mixture stirred for an additional 2 hours. The first solution was added dropwise, over a 45 minute period, to the latter solution. The resulting reaction mixture was stored overnight in a cold room. Salts were filtered from the reaction mixture and the solution was evaporated. The residue was dissolved in EtOAc (1 L) and the insoluble solids were removed by filtration. The filtrate was washed with 1x300 mL of NaHCO₃, and 2x300 mL of saturated NaCl, dried over sodium sulfate and evaporated. The residue was triturated with EtOAc to give the title compound.

10

15 2'-O-Methoxyethyl-5'-O-dimethoxytrityl-5-methylcytidine

A solution of 3'-O-acetyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyl-4-triazoleuridine (103 g, 0.141 M) in dioxane (500 mL) and NH₄OH (30 mL) was stirred at room temperature for 2 hours. The dioxane solution was evaporated and the residue azeotroped with MeOH (2x200 mL). The residue was dissolved in MeOH (300 mL) and transferred to a 2 liter stainless steel pressure vessel. MeOH (400 mL) saturated with NH₃ gas was added and the vessel heated to 100°C for 2 hours (TLC showed complete conversion). The vessel contents were evaporated to dryness and the residue was dissolved in EtOAc (500 mL) and washed once with saturated NaCl (200 mL). The organics were dried over sodium sulfate and the solvent was evaporated to give 85 g (95%) of the title compound.

20

25

N4-Benzoyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methylcytidine

2'-O-Methoxyethyl-5'-O-dimethoxytrityl-5-methylcytidine (85 g, 0.134 M) was dissolved in DMF (800 mL) and benzoic anhydride (37.2 g, 0.165 M) was added with

- 45 -

stirring. After stirring for 3 hours, TLC showed the reaction to be approximately 95% complete. The solvent was evaporated and the residue azeotroped with MeOH (200 mL). The residue was dissolved in CHCl₃ (700 mL) and extracted with saturated NaHCO₃ (2x300 mL) and saturated NaCl (2x300 mL), dried over MgSO₄ and 5 evaporated to give a residue (96 g). The residue was chromatographed on a 1.5 kg silica column using EtOAc/hexane (1:1) containing 0.5% Et₃NH as the eluting solvent. The pure product fractions were evaporated to give 90 g (90%) of the title compound.

N4-Benzoyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methylcytidine-3'-amidite

10 N4-Benzoyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methylcytidine (74 g, 0.10 M) was dissolved in CH₂Cl₂ (1 L). Tetrazole diisopropylamine (7.1 g) and 2-cyanoethoxy-tetra(isopropyl)phosphite (40.5 mL, 0.123 M) were added with stirring, under a nitrogen atmosphere. The resulting mixture was stirred for 20 hours at room temperature (TLC showed the reaction to be 95% complete). The reaction mixture 15 was extracted with saturated NaHCO₃ (1x300 mL) and saturated NaCl (3x300 mL). The aqueous washes were back-extracted with CH₂Cl₂ (300 mL), and the extracts were combined, dried over MgSO₄ and concentrated. The residue obtained was chromatographed on a 1.5 kg silica column using EtOAc/hexane (3:1) as the eluting solvent. The pure fractions were combined to give 90.6 g (87%) of the title compound.

20 **2'-O-(Aminooxyethyl) nucleoside amidites and 2'-O-(dimethylaminoxyethyl) nucleoside amidites**

2'-(Dimethylaminoxyethoxy) nucleoside amidites

25 2'-(Dimethylaminoxyethoxy) nucleoside amidites [also known in the art as 2'-O-(dimethylaminoxyethyl) nucleoside amidites] are prepared as described in the following paragraphs. Adenosine, cytidine and guanosine nucleoside amidites are prepared similarly to the thymidine (5-methyluridine) except the exocyclic amines are

- 46 -

protected with a benzoyl moiety in the case of adenosine and cytidine and with isobutyryl in the case of guanosine.

5'-O-tert-Butyldiphenylsilyl-O²-2'-anhydro-5-methyluridine

O²-2'-anhydro-5-methyluridine (Pro. Bio. Sint., Varese, Italy, 100.0g, 0.416 mmol), dimethylaminopyridine (0.66g, 0.013eq, 0.0054mmol) were dissolved in dry pyridine (500 ml) at ambient temperature under an argon atmosphere and with mechanical stirring. *tert*-Butyldiphenylchlorosilane (125.8g, 119.0mL, 1.1eq, 0.458mmol) was added in one portion. The reaction was stirred for 16 h at ambient temperature. TLC (Rf 0.22, ethyl acetate) indicated a complete reaction. The solution was concentrated under reduced pressure to a thick oil. This was partitioned between dichloromethane (1 L) and saturated sodium bicarbonate (2x1 L) and brine (1 L). The organic layer was dried over sodium sulfate and concentrated under reduced pressure to a thick oil. The oil was dissolved in a 1:1 mixture of ethyl acetate and ethyl ether (600mL) and the solution was cooled to -10°C. The resulting crystalline product was collected by filtration, washed with ethyl ether (3x200 mL) and dried (40°C, 1mm Hg, 24 h) to 149g (74.8%) of white solid. TLC and NMR were consistent with pure product.

5'-O-tert-Butyldiphenylsilyl-2'-O-(2-hydroxyethyl)-5-methyluridine

In a 2 L stainless steel, unstirred pressure reactor was added borane in tetrahydrofuran (1.0 M, 2.0 eq, 622 mL). In the fume hood and with manual stirring, ethylene glycol (350 mL, excess) was added cautiously at first until the evolution of hydrogen gas subsided. 5'-O-tert-Butyldiphenylsilyl-O²-2'-anhydro-5-methyluridine (149 g, 0.311 mol) and sodium bicarbonate (0.074 g, 0.003 eq) were added with manual stirring. The reactor was sealed and heated in an oil bath until an internal temperature of 160 °C was reached and then maintained for 16 h (pressure < 100 psig). The reaction vessel was cooled to ambient and opened. TLC (Rf 0.67 for desired product and Rf 0.82 for ara-T side product, ethyl acetate) indicated about 70% conversion to the product. In order to avoid additional side product formation, the

- 47 -

reaction was stopped, concentrated under reduced pressure (10 to 1mm Hg) in a warm water bath (40-100°C) with the more extreme conditions used to remove the ethylene glycol. [Alternatively, once the low boiling solvent is gone, the remaining solution can be partitioned between ethyl acetate and water. The product will be in the organic phase.] The residue was purified by column chromatography (2kg silica gel, ethyl acetate-hexanes gradient 1:1 to 4:1). The appropriate fractions were combined, stripped and dried to product as a white crisp foam (84g, 50%), contaminated starting material (17.4g) and pure reusable starting material 20g. The yield based on starting material less pure recovered starting material was 58%. TLC and NMR were consistent with 99% pure product.

2'-O-([2-phthalimidoxy)ethyl]-5'-*t*-butyldiphenylsilyl-5-methyluridine
5'-O-*tert*-Butyldiphenylsilyl-2'-O-(2-hydroxyethyl)-5-methyluridine (20g,
36.98mmol) was mixed with triphenylphosphine (11.63g, 44.36mmol) and N-
hydroxyphthalimide (7.24g, 44.36mmol). It was then dried over P₂O₅ under high
vacuum for two days at 40°C. The reaction mixture was flushed with argon and dry
THF (369.8mL, Aldrich, sure seal bottle) was added to get a clear solution. Diethyl-
azodicarboxylate (6.98mL, 44.36mmol) was added dropwise to the reaction mixture.
The rate of addition is maintained such that resulting deep red coloration is just
discharged before adding the next drop. After the addition was complete, the reaction
was stirred for 4 hrs. By that time TLC showed the completion of the reaction
(ethylacetate:hexane, 60:40). The solvent was evaporated in vacuum. Residue
obtained was placed on a flash column and eluted with ethyl acetate:hexane (60:40), to
get 2'-O-([2-phthalimidoxy)ethyl]-5'-*t*-butyldiphenylsilyl-5-methyluridine as white foam
(21.819 g, 86%).

25 5'-O-*tert*-butyldiphenylsilyl-2'-O-[(2-formadoximinoxy)ethyl]-5-methyluridine
2'-O-([2-phthalimidoxy)ethyl]-5'-*t*-butyldiphenylsilyl-5-methyluridine (3.1g,
4.5mmol) was dissolved in dry CH₂Cl₂ (4.5mL) and methylhydrazine (300mL,
4.64mmol) was added dropwise at -10°C to 0°C. After 1 h the mixture was filtered,

- 48 -

the filtrate was washed with ice cold CH₂Cl₂ and the combined organic phase was washed with water, brine and dried over anhydrous Na₂SO₄. The solution was concentrated to get 2'-O-(aminoxyethyl) thymidine, which was then dissolved in MeOH (67.5mL). To this formaldehyde (20% aqueous solution, w/w, 1.1 eq.) was 5 added and the resulting mixture was stirred for 1 h. Solvent was removed under vacuum; residue chromatographed to get 5'-O-*tert*-butyldiphenylsilyl-2'-O-[(2-formadoximinoxy) ethyl]-5-methyluridine as white foam (1.95 g, 78%).

5'-O-*tert*-Butyldiphenylsilyl-2'-O-[N,N-dimethylaminoxyethyl]-5-methyluridine

10 5'-O-*tert*-butyldiphenylsilyl-2'-O-[(2-formadoximinoxy)ethyl]-5-methyluridine (1.77g, 3.12mmol) was dissolved in a solution of 1M pyridinium p-toluenesulfonate (PPTS) in dry MeOH (30.6mL). Sodium cyanoborohydride (0.39g, 6.13mmol) was added to this solution at 10°C under inert atmosphere. The reaction mixture was stirred for 10 minutes at 10°C. After that the reaction vessel was removed from the ice 15 bath and stirred at room temperature for 2 h, the reaction monitored by TLC (5% MeOH in CH₂Cl₂). Aqueous NaHCO₃ solution (5%, 10mL) was added and extracted with ethyl acetate (2x20mL). Ethyl acetate phase was dried over anhydrous Na₂SO₄, evaporated to dryness. Residue was dissolved in a solution of 1M PPTS in MeOH (30.6mL). Formaldehyde (20% w/w, 30mL, 3.37mmol) was added and the reaction 20 mixture was stirred at room temperature for 10 minutes. Reaction mixture cooled to 10°C in an ice bath, sodium cyanoborohydride (0.39g, 6.13mmol) was added and reaction mixture stirred at 10°C for 10 minutes. After 10 minutes, the reaction mixture was removed from the ice bath and stirred at room temperature for 2 hrs. To the reaction mixture 5% NaHCO₃ (25mL) solution was added and extracted with ethyl acetate (2x25mL). Ethyl acetate layer was dried over anhydrous Na₂SO₄ and evaporated to dryness . The residue obtained was purified by flash column 25 chromatography and eluted with 5% MeOH in CH₂Cl₂ to get 5'-O-*tert*-butyldiphenylsilyl-2'-O-[N,N-dimethylaminoxyethyl]-5-methyluridine as a white foam (14.6g, 80%).

- 49 -

2'-O-(dimethylaminoxyethyl)-5-methyluridine

Triethylamine trihydrofluoride (3.91mL, 24.0mmol) was dissolved in dry THF and triethylamine (1.67mL, 12mmol, dry, kept over KOH). This mixture of triethylamine-2HF was then added to 5'-O-*tert*-butyldiphenylsilyl-2'-O-[N,N-dimethylaminoxyethyl]-5-methyluridine (1.40g, 2.4mmol) and stirred at room temperature for 24 hrs. Reaction was monitored by TLC (5% MeOH in CH₂Cl₂). Solvent was removed under vacuum and the residue placed on a flash column and eluted with 10% MeOH in CH₂Cl₂ to get 2'-O-(dimethylaminoxyethyl)-5-methyluridine (766mg, 92.5%).

10 **5'-O-DMT-2'-O-(dimethylaminoxyethyl)-5-methyluridine**

2'-O-(dimethylaminoxyethyl)-5-methyluridine (750mg, 2.17mmol) was dried over P₂O₅ under high vacuum overnight at 40°C. It was then co-evaporated with anhydrous pyridine (20mL). The residue obtained was dissolved in pyridine (11mL) under argon atmosphere. 4-dimethylaminopyridine (26.5mg, 2.60mmol), 4,4'-dimethoxytrityl chloride (880mg, 2.60mmol) was added to the mixture and the reaction mixture was stirred at room temperature until all of the starting material disappeared. Pyridine was removed under vacuum and the residue chromatographed and eluted with 10% MeOH in CH₂Cl₂ (containing a few drops of pyridine) to get 5'-O-DMT-2'-O-(dimethylamino-oxyethyl)-5-methyluridine (1.13g, 80%).

20 **5'-O-DMT-2'-O-(2-N,N-dimethylaminoxyethyl)-5-methyluridine-3'-(2-cyanoethyl)-N,N-diisopropylphosphoramidite]**

5'-O-DMT-2'-O-(dimethylaminoxyethyl)-5-methyluridine (1.08g, 1.67mmol) was co-evaporated with toluene (20mL). To the residue N,N-diisopropylamine tetrazonide (0.29g, 1.67mmol) was added and dried over P₂O₅ under high vacuum overnight at 40°C. Then the reaction mixture was dissolved in anhydrous acetonitrile (8.4mL) and 2-cyanoethyl-N,N,N¹,N¹-tetraisopropylphosphoramidite (2.12mL, 6.08mmol) was added. The reaction mixture was stirred at ambient temperature for 4 hrs under inert atmosphere. The progress of the reaction was monitored by TLC

- 50 -

(hexane:ethyl acetate 1:1). The solvent was evaporated, then the residue was dissolved in ethyl acetate (70mL) and washed with 5% aqueous NaHCO₃ (40mL). Ethyl acetate layer was dried over anhydrous Na₂SO₄ and concentrated. Residue obtained was chromatographed (ethyl acetate as eluent) to get 5'-O-DMT-2'-O-(2-N,N-dimethylaminoxyethyl)-5-methyluridine-3'-[(2-cyanoethyl)-N,N-diisopropylphosphoramidite] as a foam (1.04g, 74.9%).

2'- (Aminooxyethoxy) nucleoside amidites

2'- (Aminooxyethoxy) nucleoside amidites [also known in the art as 2'-O-(aminooxyethyl) nucleoside amidites] are prepared as described in the following 10 paragraphs. Adenosine, cytidine and thymidine nucleoside amidites are prepared similarly.

N2-isobutyryl-6-O-diphenylcarbamoyl-2'-O-(2-ethylacetyl)-5'-O-(4,4'-dimethoxytrityl)guanosine-3'-[(2-cyanoethyl)-N,N-diisopropylphosphoramidite]

The 2'-O-aminooxyethyl guanosine analog may be obtained by selective 2'-O-alkylation of diaminopurine riboside. Multigram quantities of diaminopurine riboside may be purchased from Schering AG (Berlin) to provide 2'-O-(2-ethylacetyl) diaminopurine riboside along with a minor amount of the 3'-O-isomer. 2'-O-(2-ethylacetyl) diaminopurine riboside may be resolved and converted to 2'-O-(2-ethylacetyl)guanosine by treatment with adenosine deaminase. (McGee, D. P. C., Cook, P. D., Guinossio, C. J., WO 94/02501 A1 940203.) Standard protection procedures should afford 2'-O-(2-ethylacetyl)-5'-O-(4,4'-dimethoxytrityl)guanosine and 2-N-isobutyryl-6-O-diphenylcarbamoyl-2'-O-(2-ethylacetyl)-5'-O-(4,4'-dimethoxytrityl)guanosine which may be reduced to provide 2-N-isobutyryl-6-O-diphenylcarbamoyl-2'-O-(2-ethylacetyl)-5'-O-(4,4'-dimethoxytrityl)guanosine. As before 25 the hydroxyl group may be displaced by N-hydroxypythalimide via a Mitsunobu reaction, and the protected nucleoside may phosphitylated as usual to yield 2-N-

This Page Blank (uspto)

- 51 -

isobutyryl-6-O-diphenylcarbamoyl-2'-O-(2-ethylacetyl)-5'-O-(4,4'-dimethoxytrityl)guanosine-3'-(2-cyanoethyl)-N,N-diisopropylphosphoramidite].

2'-dimethylaminoethoxyethoxy (2'-DMAEOE) nucleoside amidites

5 2'-dimethylaminoethoxyethoxy nucleoside amidites (also known in the art as 2'-O-dimethylaminoethoxyethyl, i.e., 2'-O-CH₂-O-CH₂-N(CH₃)₂, or 2'-DMAEOE nucleoside amidites) are prepared as follows. Other nucleoside amidites are prepared similarly.

2'-O-[2(2-N,N-dimethylaminoethoxy)ethyl]-5-methyl uridine

10 2[2-(Dimethylamino)ethoxy]ethanol (Aldrich, 6.66 g, 50 mmol) is slowly added to a solution of borane in tetrahydrofuran (1 M, 10 mL, 10 mmol) with stirring in a 100 mL bomb. Hydrogen gas evolves as the solid dissolves. O²⁻,2'-anhydro-5-methyluridine (1.2 g, 5 mmol), and sodium bicarbonate (2.5 mg) are added and the bomb is sealed, placed in an oil bath and heated to 155 °C for 26 hours. The bomb is cooled to room temperature and opened. The crude solution is concentrated and the residue 15 partitioned between water (200 mL) and hexanes (200 mL). The excess phenol is extracted into the hexane layer. The aqueous layer is extracted with ethyl acetate (3x200 mL) and the combined organic layers are washed once with water, dried over anhydrous sodium sulfate and concentrated. The residue is columned on silica gel using methanol/methylene chloride 1:20 (which has 2% triethylamine) as the eluent. As 20 the column fractions are concentrated a colorless solid forms which is collected to give the title compound as a white solid.

5'-O-dimethoxytrityl-2'-O-[2(2-N,N-dimethylaminoethoxy)ethyl]-5-methyl uridine

25 To 0.5 g (1.3 mmol) of 2'-O-[2(2-N,N-dimethylaminoethoxy)ethyl]-5-methyl uridine in anhydrous pyridine (8 mL), triethylamine (0.36 mL) and dimethoxytrityl chloride (DMT-Cl, 0.87 g, 2 eq.) are added and stirred for 1 hour. The reaction mixture is poured into water (200 mL) and extracted with CH₂Cl₂ (2x200 mL). The

- 52 -

combined CH_2Cl_2 layers are washed with saturated NaHCO_3 solution, followed by saturated NaCl solution and dried over anhydrous sodium sulfate. Evaporation of the solvent followed by silica gel chromatography using $\text{MeOH}:\text{CH}_2\text{Cl}_2:\text{Et}_3\text{N}$ (20:1, v/v, with 1% triethylamine) gives the title compound.

5 5'-O-Dimethoxytrityl-2'-O-[2(2-N,N-dimethylaminoethoxy)ethyl])-5-methyl uridine-3'-O-(cyanoethyl-N,N-diisopropyl)phosphoramidite
Diisopropylaminotetrazolide (0.6 g) and 2-cyanoethoxy-N,N-diisopropyl
10 phosphoramidite (1.1 mL, 2 eq.) are added to a solution of 5'-O-dimethoxytrityl-2'-O-[2(2-N,N-dimethylaminoethoxy)ethyl])-5-methyluridine (2.17 g, 3 mmol) dissolved in
15 CH_2Cl_2 (20 mL) under an atmosphere of argon. The reaction mixture is stirred
overnight and the solvent evaporated. The resulting residue is purified by silica gel
flash column chromatography with ethyl acetate as the eluent to give the title
compound.

Example 2

15 Oligonucleotide synthesis

Unsubstituted and substituted phosphodiester ($\text{P}=\text{O}$) oligonucleotides are synthesized on an automated DNA synthesizer (Applied Biosystems model 380B) using standard phosphoramidite chemistry with oxidation by iodine.

20 Phosphorothioates ($\text{P}=\text{S}$) are synthesized as for the phosphodiester oligonucleotides except the standard oxidation bottle was replaced by 0.2 M solution of 3H-1,2-benzodithiole-3-one 1,1-dioxide in acetonitrile for the stepwise thiation of the phosphite linkages. The thiation wait step was increased to 68 sec and was followed by the capping step. After cleavage from the CPG column and deblocking in concentrated ammonium hydroxide at 55°C (18 h), the oligonucleotides were purified by precipitating twice with 2.5 volumes of ethanol from a 0.5 M NaCl solution.
25 Phosphinate oligonucleotides are prepared as described in U.S. Patent 5,508,270, herein incorporated by reference.

- 53 -

Alkyl phosphonate oligonucleotides are prepared as described in U.S. Patent 4,469,863, herein incorporated by reference.

3'-Deoxy-3'-methylene phosphonate oligonucleotides are prepared as described in U.S. Patents 5,610,289 or 5,625,050, herein incorporated by reference.

5 Phosphoramidite oligonucleotides are prepared as described in U.S. Patent, 5,256,775 or U.S. Patent 5,366,878, herein incorporated by reference.

Alkylphosphonothioate oligonucleotides are prepared as described in published PCT applications PCT/US94/00902 and PCT/US93/06976 (published as WO 94/17093 and WO 94/02499, respectively), herein incorporated by reference.

10 3'-Deoxy-3'-amino phosphoramidate oligonucleotides are prepared as described in U.S. Patent 5,476,925, herein incorporated by reference.

11 Phosphotriester oligonucleotides are prepared as described in U.S. Patent 5,023,243, herein incorporated by reference.

Borano phosphate oligonucleotides are prepared as described in U.S. Patents 15 5,130,302 and 5,177,198, both herein incorporated by reference.

Example 3

Oligonucleoside Synthesis

Methylenemethylimino linked oligonucleosides, also identified as MMI linked oligonucleosides, methylenedimethylhydrazo linked oligonucleosides, also identified as 20 MDH linked oligonucleosides, and methylenecarbonylamino linked oligonucleosides, also identified as amide-3 linked oligonucleosides, and methyleneaminocarbonyl linked oligonucleosides, also identified as amide-4 linked oligonucleosides, as well as mixed backbone compounds having, for instance, alternating MMI and P=O or P=S linkages are prepared as described in U.S. Patents 5,378,825, 5,386,023, 5,489,677, 5,602,240 and 5,610,289, all of which are herein incorporated by reference.

25 Formacetal and thioformacetal linked oligonucleosides are prepared as described in U.S. Patents 5,264,562 and 5,264,564, herein incorporated by reference.

Ethylene oxide linked oligonucleosides are prepared as described in U.S. Patent 5,223,618, herein incorporated by reference.

- 54 -

Example 4

PNA Synthesis

Peptide nucleic acids (PNAs) are prepared in accordance with any of the various procedures referred to in Peptide Nucleic Acids (PNA): Synthesis, Properties and Potential Applications, *Bioorganic & Medicinal Chemistry*, 1996, 4, 5-23. They 5 may also be prepared in accordance with U.S. Patents 5,539,082, 5,700,922, and 5,719,262, herein incorporated by reference.

Example 5

Synthesis of Chimeric Oligonucleotides

Chimeric oligonucleotides, oligonucleosides or mixed 10 oligonucleotides/oligonucleosides of the invention can be of several different types. These include a first type wherein the "gap" segment of linked nucleosides is positioned between 5' and 3' "wing" segments of linked nucleosides and a second "open end" type wherein the "gap" segment is located at either the 3' or the 5' terminus of the oligomeric 15 compound. Oligonucleotides of the first type are also known in the art as "gapmers" or gapped oligonucleotides. Oligonucleotides of the second type are also known in the art as "hemimers" or "wingmers".

[2'-O-Me]--[2'-deoxy]--[2'-O-Me] Chimeric Phosphorothioate

Oligonucleotides

Chimeric oligonucleotides having 2'-O-alkyl phosphorothioate and 2'-deoxy 20 phosphorothioate oligonucleotide segments are synthesized using an Applied Biosystems automated DNA synthesizer Model 380B, as above. Oligonucleotides are synthesized using the automated synthesizer and 2'-deoxy-5'-dimethoxytrityl-3'-O-phosphoramidite for the DNA portion and 5'-dimethoxytrityl-2'-O-methyl-3'-O-phosphoramidite for 5' and 3' wings. The standard synthesis cycle is modified by increasing the wait step after the delivery of tetrazole and base to 600 s repeated four 25 times for RNA and twice for 2'-O-methyl. The fully protected oligonucleotide is cleaved from the support and the phosphate group is deprotected in 3:1 ammonia/ethanol at room temperature overnight then lyophilized to dryness.

- 55 -

Treatment in methanolic ammonia for 24 hrs at room temperature is then done to deprotect all bases and sample was again lyophilized to dryness. The pellet is resuspended in 1M TBAF in THF for 24 hrs at room temperature to deprotect the 2' positions. The reaction is then quenched with 1M TEAA and the sample is then 5 reduced to 1/2 volume by rotovac before being desalted on a G25 size exclusion column. The oligo recovered is then analyzed spectrophotometrically for yield and for purity by capillary electrophoresis and by mass spectrometry.

**[2'-O-(2-Methoxyethyl)]-[2'-deoxy]-[2'-O-(Methoxyethyl)] Chimeric
Phosphorothioate Oligonucleotides**

10 [2'-O-(2-methoxyethyl)]-[2'-deoxy]-[-2'-O-(methoxyethyl)] chimeric phosphorothioate oligonucleotides were prepared as per the procedure above for the 2'-O-methyl chimeric oligonucleotide, with the substitution of 2'-O-(methoxyethyl) amidites for the 2'-O-methyl amidites.

15 **[2'-O-(2-Methoxyethyl)Phosphodiester]-[2'-deoxy Phosphorothioate]-[2'-
O-(2-Methoxyethyl) Phosphodiester] Chimeric Oligonucleotides**
[2'-O-(2-methoxyethyl phosphodiester]-[2'-deoxy phosphorothioate]-[2'-O-(methoxyethyl) phosphodiester] chimeric oligonucleotides are prepared as per the above procedure for the 2'-O-methyl chimeric oligonucleotide with the substitution of 2'-O-(methoxyethyl) amidites for the 2'-O-methyl amidites, oxidation with iodine to 20 generate the phosphodiester internucleotide linkages within the wing portions of the chimeric structures and sulfurization utilizing 3,H-1,2 benzodithiole-3-one 1,1 dioxide (Beaucage Reagent) to generate the phosphorothioate internucleotide linkages for the center gap.

25 Other chimeric oligonucleotides, chimeric oligonucleosides and mixed chimeric oligonucleotides/oligonucleosides are synthesized according to United States patent 5,623,065, herein incorporated by reference.

- 56 -

Example 6

Oligonucleotide Isolation

After cleavage from the controlled pore glass column (Applied Biosystems) and deblocking in concentrated ammonium hydroxide at 55°C for 18 hours, the 5 oligonucleotides or oligonucleosides are purified by precipitation twice out of 0.5 M NaCl with 2.5 volumes ethanol. Synthesized oligonucleotides were analyzed by polyacrylamide gel electrophoresis on denaturing gels and judged to be at least 85% full length material. The relative amounts of phosphorothioate and phosphodiester linkages obtained in synthesis were periodically checked by ³¹P nuclear magnetic resonance 10 spectroscopy, and for some studies oligonucleotides were purified by HPLC, as described by Chiang et al., *J. Biol. Chem.* 1991, 266, 18162-18171. Results obtained with HPLC-purified material were similar to those obtained with non-HPLC purified material.

Example 7

15 **Oligonucleotide Synthesis - 96 Well Plate Format**

Oligonucleotides were synthesized via solid phase P(III) phosphoramidite chemistry on an automated synthesizer capable of assembling 96 sequences simultaneously in a standard 96 well format. Phosphodiester internucleotide linkages were afforded by oxidation with aqueous iodine. Phosphorothioate internucleotide 20 linkages were generated by sulfurization utilizing 3,H-1,2 benzodithiole-3-one 1,1 dioxide (Beaucage Reagent) in anhydrous acetonitrile. Standard base-protected beta-cyanoethyldiisopropyl phosphoramidites were purchased from commercial vendors (e.g. PE-Applied Biosystems, Foster City, CA, or Pharmacia, Piscataway, NJ). Non-standard nucleosides are synthesized as per known literature or patented methods. 25 They are utilized as base protected beta-cyanoethyldiisopropyl phosphoramidites.

Oligonucleotides were cleaved from support and deprotected with concentrated NH₄OH at elevated temperature (55-60°C) for 12-16 hours and the released product then dried in vacuo. The dried product was then re-suspended in sterile water to afford

- 57 -

a master plate from which all analytical and test plate samples are then diluted utilizing robotic pipettors.

Example 8

Oligonucleotide Analysis - 96 Well Plate Format

5 The concentration of oligonucleotide in each well was assessed by dilution of samples and UV absorption spectroscopy. The full-length integrity of the individual products was evaluated by capillary electrophoresis (CE) in either the 96 well format (Beckman P/ACE™ MDQ) or, for individually prepared samples, on a commercial CE apparatus (e.g., Beckman P/ACE™ 5000, ABI 270). Base and backbone composition
10 was confirmed by mass analysis of the compounds utilizing electrospray-mass spectroscopy. All assay test plates were diluted from the master plate using single and multi-channel robotic pipettors. Plates were judged to be acceptable if at least 85% of the compounds on the plate were at least 85% full length.

Example 9

15 **Cell culture and oligonucleotide treatment**

 The effect of antisense compounds on target nucleic acid expression can be tested in any of a variety of cell types provided that the target nucleic acid is present at measurable levels. This can be routinely determined using, for example, PCR or Northern blot analysis. The following 5 cell types are provided for illustrative purposes, but other cell types can be routinely used, provided that the target is expressed in the cell type chosen. This can be readily determined by methods routine in the art, for example Northern blot analysis, Ribonuclease protection assays, or RT-PCR.

T-24 cells:

25 The human transitional cell bladder carcinoma cell line T-24 was obtained from the American Type Culture Collection (ATCC) (Manassas, VA). T-24 cells were routinely cultured in complete McCoy's 5A basal media (Gibco/Life Technologies,

- 58 -

Gaithersburg, MD) supplemented with 10% fetal calf serum (Gibco/Life Technologies, Gaithersburg, MD), penicillin 100 units per mL, and streptomycin 100 micrograms per mL (Gibco/Life Technologies, Gaithersburg, MD). Cells were routinely passaged by trypsinization and dilution when they reached 90% confluence. Cells were seeded into 5 96-well plates (Falcon-Primaria #3872) at a density of 7000 cells/well for use in RT-PCR analysis.

For Northern blotting or other analysis, cells may be seeded onto 100 mm or other standard tissue culture plates and treated similarly, using appropriate volumes of medium and oligonucleotide.

10 A549 cells:

The human lung carcinoma cell line A549 was obtained from the American Type Culture Collection (ATCC) (Manassas, VA). A549 cells were routinely cultured in DMEM basal media (Gibco/Life Technologies, Gaithersburg, MD) supplemented with 10% fetal calf serum (Gibco/Life Technologies, Gaithersburg, MD), penicillin 100 15 units per mL, and streptomycin 100 micrograms per mL (Gibco/Life Technologies, Gaithersburg, MD). Cells were routinely passaged by trypsinization and dilution when they reached 90% confluence.

NHDF cells:

Human neonatal dermal fibroblast (NHDF) were obtained from the Clonetics Corporation (Walkersville MD). NHDFs were routinely maintained in Fibroblast Growth Medium (Clonetics Corporation, Walkersville MD) supplemented as recommended by the supplier. Cells were maintained for up to 10 passages as 20 recommended by the supplier.

HEK cells:

Human embryonic keratinocytes (HEK) were obtained from the Clonetics Corporation (Walkersville MD). HEKs were routinely maintained in Keratinocyte Growth Medium (Clonetics Corporation, Walkersville MD) formulated as 25

- 59 -

recommended by the supplier. Cells were routinely maintained for up to 10 passages as recommended by the supplier.

PC-12 cells:

The rat neuronal cell line PC-12 was obtained from the American Type Culture Collection (Manassas, VA). PC-12 cells were routinely cultured in DMEM, high glucose (Gibco/Life Technologies, Gaithersburg, MD) supplemented with 10% horse serum + 5% fetal calf serum (Gibco/Life Technologies, Gaithersburg, MD). Cells were routinely passaged by trypsinization and dilution when they reached 90% confluence. Cells were seeded into 96-well plates (Falcon-Primaria #3872) at a density of 20000 cells/well for use in RT-PCR analysis.

For Northern blotting or other analysis, cells may be seeded onto 100 mm or other standard tissue culture plates and treated similarly, using appropriate volumes of medium and oligonucleotide.

Treatment with antisense compounds:

When cells reached 80% confluency, they were treated with oligonucleotide. For cells grown in 96-well plates, wells were washed once with 200 µL OPTI-MEM™-1 reduced-serum medium (Gibco BRL) and then treated with 130 µL of OPTI-MEM™-1 containing 3.75 µg/mL LIPOFECTIN™ (Gibco BRL) and the desired concentration of oligonucleotide. After 4-7 hours of treatment, the medium was replaced with fresh medium. Cells were harvested 16-24 hours after oligonucleotide treatment.

The concentration of oligonucleotide used varies from cell line to cell line. To determine the optimal oligonucleotide concentration for a particular cell line, the cells are treated with a positive control oligonucleotide at a range of concentrations. For human cells the positive control oligonucleotide is ISIS 13920, TCCGTCATCGCTCCTCAGGG, SEQ ID NO: 1, a 2'-O-methoxyethyl gapmer (2'-O-methoxyethyls shown in bold) with a phosphorothioate backbone which is targeted to human H-ras. For mouse or rat cells the positive control oligonucleotide is ISIS

- 60 -

15770, ATGCATTCTGCCCAAGGA, SEQ ID NO: 2, a 2'-O-methoxyethyl gapmer (2'-O-methoxyethyls shown in bold) with a phosphorothioate backbone which is targeted to both mouse and rat c-raf. The concentration of positive control oligonucleotide that results in 80% inhibition of c-Ha-ras (for ISIS 13920) or c-raf (for 5 ISIS 15770) mRNA is then utilized as the screening concentration for new oligonucleotides in subsequent experiments for that cell line. If 80% inhibition is not achieved, the lowest concentration of positive control oligonucleotide that results in 60% inhibition of H-ras or c-raf mRNA is then utilized as the oligonucleotide screening concentration in subsequent experiments for that cell line. If 60% inhibition is not 10 achieved, that particular cell line is deemed as unsuitable for oligonucleotide transfection experiments.

Example 10

Analysis of oligonucleotide inhibition of PTP1B expression

Antisense modulation of PTP1B expression can be assayed in a variety of ways known in the art. For example, PTP1B mRNA levels can be quantitated by, e.g., Northern blot analysis, competitive polymerase chain reaction (PCR), or real-time PCR (RT-PCR). Real-time quantitative PCR is presently preferred. RNA analysis can be performed on total cellular RNA or poly(A)+ mRNA. Methods of RNA isolation are taught in, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, 15 Volume 1, pp. 4.1.1-4.2.9 and 4.5.1-4.5.3, John Wiley & Sons, Inc., 1993. Northern blot analysis is routine in the art and is taught in, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 1, pp. 4.2.1-4.2.9, John Wiley & Sons, Inc., 1996. Real-time quantitative (PCR) can be conveniently accomplished 20 using the commercially available ABI PRISM™ 7700 Sequence Detection System, available from PE-Applied Biosystems, Foster City, CA and used according to manufacturer's instructions. Prior to quantitative PCR analysis, primer-probe sets specific to the target gene being measured are evaluated for their ability to be 25 "multiplexed" with a GAPDH amplification reaction. In multiplexing, both the target gene and the internal standard gene GAPDH are amplified concurrently in a single

- 61 -

sample. In this analysis, mRNA isolated from untreated cells is serially diluted. Each dilution is amplified in the presence of primer-probe sets specific for GAPDH only, target gene only ("single-plexing"), or both (multiplexing). Following PCR amplification, standard curves of GAPDH and target mRNA signal as a function of dilution are generated from both the single-plexed and multiplexed samples. If both the slope and correlation coefficient of the GAPDH and target signals generated from the multiplexed samples fall within 10% of their corresponding values generated from the single-plexed samples, the primer-probe set specific for that target is deemed as multiplexable. Other methods of PCR are also known in the art.

10 Protein levels of PTP1B can be quantitated in a variety of ways well known in the art, such as immunoprecipitation, Western blot analysis (immunoblotting), ELISA or fluorescence-activated cell sorting (FACS). Antibodies directed to PTP1B can be identified and obtained from a variety of sources, such as the MSRS catalog of antibodies (Aerie Corporation, Birmingham, MI), or can be prepared via conventional antibody generation methods. Methods for preparation of polyclonal antisera are taught in, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 2, pp. 11.12.1-11.12.9, John Wiley & Sons, Inc., 1997. Preparation of monoclonal antibodies is taught in, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 2, pp. 11.4.1-11.11.5, John Wiley & Sons, Inc., 1997.

15 Immunoprecipitation methods are standard in the art and can be found at, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 2, pp. 10.16.1-10.16.11, John Wiley & Sons, Inc., 1998. Western blot (immunoblot) analysis is standard in the art and can be found at, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 2, pp. 10.8.1-10.8.21, John Wiley & Sons, Inc., 1997. Enzyme-linked immunosorbent assays (ELISA) are standard in the art and can be found at, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 2, pp. 11.2.1-11.2.22, John Wiley & Sons, Inc., 1991.

- 62 -

Example 11

Poly(A)+ mRNA isolation

Poly(A)+ mRNA was isolated according to Miura et al., *Clin. Chem.*, 1996, 42, 1758-1764. Other methods for poly(A)+ mRNA isolation are taught in, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 1, pp. 4.5.1-4.5.3, John Wiley & Sons, Inc., 1993. Briefly, for cells grown on 96-well plates, growth medium was removed from the cells and each well was washed with 200 µL cold PBS. 60 µL lysis buffer (10 mM Tris-HCl, pH 7.6, 1 mM EDTA, 0.5 M NaCl, 0.5% NP-40, 20 mM vanadyl-ribonucleoside complex) was added to each well, the plate was gently agitated and then incubated at room temperature for five minutes. 55 10 µL of lysate was transferred to Oligo d(T) coated 96-well plates (AGCT Inc., Irvine CA). Plates were incubated for 60 minutes at room temperature, washed 3 times with 200 µL of wash buffer (10 mM Tris-HCl pH 7.6, 1 mM EDTA, 0.3 M NaCl). After the final wash, the plate was blotted on paper towels to remove excess wash buffer and 15 then air-dried for 5 minutes. 60 µL of elution buffer (5 mM Tris-HCl pH 7.6), preheated to 70°C was added to each well, the plate was incubated on a 90°C hot plate for 5 minutes, and the eluate was then transferred to a fresh 96-well plate.

Cells grown on 100 mm or other standard plates may be treated similarly, using appropriate volumes of all solutions.

20 **Example 12**

Total RNA Isolation

Total mRNA was isolated using an RNEASY 96™ kit and buffers purchased from Qiagen Inc. (Valencia CA) following the manufacturer's recommended procedures. Briefly, for cells grown on 96-well plates, growth medium was removed 25 from the cells and each well was washed with 200 µL cold PBS. 100 µL Buffer RLT was added to each well and the plate vigorously agitated for 20 seconds. 100 µL of 70% ethanol was then added to each well and the contents mixed by pipetting three times up and down. The samples were then transferred to the RNEASY 96™ well plate attached to a QIAVAC™ manifold fitted with a waste collection tray and

- 63 -

attached to a vacuum source. Vacuum was applied for 15 seconds. 1 mL of Buffer RW1 was added to each well of the RNEASY 96™ plate and the vacuum again applied for 15 seconds. 1 mL of Buffer RPE was then added to each well of the RNEASY 96™ plate and the vacuum applied for a period of 15 seconds. The Buffer RPE wash 5 was then repeated and the vacuum was applied for an additional 10 minutes. The plate was then removed from the QIAVAC™ manifold and blotted dry on paper towels. The plate was then re-attached to the QIAVAC™ manifold fitted with a collection tube rack containing 1.2 mL collection tubes. RNA was then eluted by pipetting 60 µL water into each well, incubating 1 minute, and then applying the vacuum for 30 10 seconds. The elution step was repeated with an additional 60 µL water.

The repetitive pipetting and elution steps may be automated using a QIAGEN Bio-Robot 9604 (Qiagen, Inc., Valencia CA). Essentially, after lysing of the cells on the culture plate, the plate is transferred to the robot deck where the pipetting, DNase treatment and elution steps are carried out.

15 **Example 13**

Real-time Quantitative PCR Analysis of PTP1B mRNA Levels

Quantitation of PTP1B mRNA levels was determined by real-time quantitative PCR using the ABI PRISM™ 7700 Sequence Detection System (PE-Applied Biosystems, Foster City, CA) according to manufacturer's instructions. This is a 20 closed-tube, non-gel-based, fluorescence detection system which allows high-throughput quantitation of polymerase chain reaction (PCR) products in real-time. As opposed to standard PCR, in which amplification products are quantitated after the PCR is completed, products in real-time quantitative PCR are quantitated as they accumulate. This is accomplished by including in the PCR reaction an oligonucleotide probe that anneals specifically between the forward and reverse PCR primers, and 25 contains two fluorescent dyes. A reporter dye (e.g., JOE, FAM, or VIC, obtained from either Operon Technologies Inc., Alameda, CA or PE-Applied Biosystems, Foster City, CA) is attached to the 5' end of the probe and a quencher dye (e.g., TAMRA, obtained from either Operon Technologies Inc., Alameda, CA or PE-Applied Biosystems, Foster

- 64 -

City, CA) is attached to the 3' end of the probe. When the probe and dyes are intact, reporter dye emission is quenched by the proximity of the 3' quencher dye. During amplification, annealing of the probe to the target sequence creates a substrate that can be cleaved by the 5'-exonuclease activity of Taq polymerase. During the extension 5 phase of the PCR amplification cycle, cleavage of the probe by Taq polymerase releases the reporter dye from the remainder of the probe (and hence from the quencher moiety) and a sequence-specific fluorescent signal is generated. With each cycle, additional reporter dye molecules are cleaved from their respective probes, and the fluorescence intensity is monitored at regular intervals by laser optics built into the ABI PRISM™ 10 7700 Sequence Detection System. In each assay, a series of parallel reactions containing serial dilutions of mRNA from untreated control samples generates a standard curve that is used to quantitate the percent inhibition after antisense oligonucleotide treatment of test samples.

PCR reagents were obtained from PE-Applied Biosystems, Foster City, CA. 15 RT-PCR reactions were carried out by adding 25 µL PCR cocktail (1x TAQMAN™ buffer A, 5.5 mM MgCl₂, 300 µM each of dATP, dCTP and dGTP, 600 µM of dUTP, 100 nM each of forward primer, reverse primer, and probe, 20 Units RNase inhibitor, 1.25 Units AMPLITAQ GOLD™, and 12.5 Units MuLV reverse transcriptase) to 96 well plates containing 25 µL poly(A) mRNA solution. The RT reaction was carried 20 out by incubation for 30 minutes at 48°C. Following a 10 minute incubation at 95°C to activate the AMPLITAQ GOLD™, 40 cycles of a two-step PCR protocol were carried out: 95°C for 15 seconds (denaturation) followed by 60°C for 1.5 minutes (annealing/extension).

Probes and primers to human PTP1B were designed to hybridize to a human 25 PTP1B sequence, using published sequence information (GenBank accession number M31724, incorporated herein as SEQ ID NO:3). For human PTP1B the PCR primers were:

forward primer: GGAGTCGAGCAGATCGACAA (SEQ ID NO: 4)
reverse primer: GGCCACTCTACATGGGAAGTC (SEQ ID NO: 5) and the PCR
30 probe was: FAM-AGCTGGCGGCCATTACCAGGAT-TAMRA

- 65 -

(SEQ ID NO: 6) where FAM (PE-Applied Biosystems, Foster City, CA) is the fluorescent reporter dye) and TAMRA (PE-Applied Biosystems, Foster City, CA) is the quencher dye. For human GAPDH the PCR primers were:

forward primer: GAAGGTGAAGGTCGGAGTC (SEQ ID NO: 7)

5 reverse primer: GAAGATGGTGATGGGATTTC (SEQ ID NO: 8) and the PCR probe was: 5' JOE-CAAGCTTCCCGTTCTCAGCC- TAMRA 3' (SEQ ID NO: 9) where JOE (PE-Applied Biosystems, Foster City, CA) is the fluorescent reporter dye) and TAMRA (PE-Applied Biosystems, Foster City, CA) is the quencher dye.

Probes and primers to rat PTP1B were designed to hybridize to a rat PTP1B sequence, using published sequence information (GenBank accession number M33962, incorporated herein as SEQ ID NO:10). For rat PTP1B the PCR primers were:

forward primer: CGAGGGTGCAAAGTTCATCAT (SEQ ID NO:11)

reverse primer: CCAGGTCTTCATGGGAAAGCT (SEQ ID NO: 12) and the PCR probe was: FAM-CGACTCGTCAGTGCAGGATCAGTGGTA-TAMRA

15 (SEQ ID NO: 13) where FAM (PE-Applied Biosystems, Foster City, CA) is the fluorescent reporter dye) and TAMRA (PE-Applied Biosystems, Foster City, CA) is the quencher dye. For rat GAPDH the PCR primers were:

forward primer: TGTTCTAGAGACAGCCGCATCTT (SEQ ID NO: 14)

reverse primer: CACCGACCTTCACCACATCTTGT (SEQ ID NO: 15) and the PCR probe was: 5' JOE-TTGTGCAGTGCCAGCCTCGTCTCA- TAMRA 3' (SEQ ID NO: 16) where JOE (PE-Applied Biosystems, Foster City, CA) is the fluorescent reporter dye) and TAMRA (PE-Applied Biosystems, Foster City, CA) is the quencher dye.

Example 14

Northern blot analysis of PTP1B mRNA levels

25 Eighteen hours after antisense treatment, cell monolayers were washed twice with cold PBS and lysed in 1 mL RNAZOL™ (TEL-TEST "B" Inc., Friendswood, TX). Total RNA was prepared following manufacturer's recommended protocols. Twenty micrograms of total RNA was fractionated by electrophoresis through 1.2% agarose gels containing 1.1% formaldehyde using a MOPS buffer system (AMRESCO,

- 66 -

Inc. Solon, OH). RNA was transferred from the gel to HYBOND™-N+ nylon membranes (Amersham Pharmacia Biotech, Piscataway, NJ) by overnight capillary transfer using a Northern/Southern Transfer buffer system (TEL-TEST "B" Inc., Friendswood, TX). RNA transfer was confirmed by UV visualization. Membranes 5 were fixed by UV cross-linking using a STRATALINKER™ UV Crosslinker 2400 (Stratagene, Inc, La Jolla, CA) and then robed using QUICKHYB™ hybridization solution (Stratagene, La Jolla, CA) using manufacturer's recommendations for stringent conditions.

To detect human PTP1B, a human PTP1B specific probe was prepared by PCR 10 using the forward primer GGAGITCGAGCAGATCGACAA (SEQ ID NO: 4) and the reverse primer GGCCACTCTACATGGGAAGTC (SEQ ID NO: 5). To normalize for variations in loading and transfer efficiency membranes were stripped and probed for human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) RNA (Clontech, Palo Alto, CA).

To detect rat PTP1B, a rat PTP1B specific probe was prepared by PCR using 15 the forward primer CGAGGGTGCAAAGTTCATCAT (SEQ ID NO:11) and the reverse primer CCAGGTCTTCATGGAAAGCT (SEQ ID NO: 12). To normalize for variations in loading and transfer efficiency membranes were stripped and probed for rat glyceraldehyde-3-phosphate dehydrogenase (GAPDH) RNA (Clontech, Palo Alto, CA).

Hybridized membranes were visualized and quantitated using a PHOSPHORIMAGER™ and IMAGEQUANT™ Software V3.3 (Molecular Dynamics, Sunnyvale, CA). Data was normalized to GAPDH levels in untreated controls.

25 **Example 15**

Antisense inhibition of human PTP1B expression by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap

In accordance with the present invention, a series of oligonucleotides were designed to target different regions of the human PTP1B RNA, using published

- 67 -

sequences (GenBank accession number M31724, incorporated herein as SEQ ID NO: 3). The oligonucleotides are shown in Table 1. "Target site" indicates the first (5'-most) nucleotide number on the particular target sequence to which the oligonucleotide binds. All compounds in Table 1 are chimeric oligonucleotides ("gapmers") 20 5 nucleotides in length, composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings". The wings are composed of 2'-methoxyethyl (2'-MOE)nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. All cytidine residues are 5-methylcytidines. The compounds were 10 analyzed for their effect on human PTP1B mRNA levels by quantitative real-time PCR as described in other examples herein. Data are averages from two experiments. If present, "N.D." indicates "no data".

Table 1
Inhibition of human PTP1B mRNA levels by chimeric phosphorothioate
15 oligonucleotides having 2'-MOE wings and a deoxy gap

ISIS #	REGION	TARGET SEQ ID NO	TARGET SITE	SEQUENCE	% INHIB	SEQ ID NO
107769	5' UTR	3	1	cttagcccgaggccccgccc	0	17
107770	5' UTR	3	41	ctcgcccaactgcggcgct	58	18
107771	Start Codon	3	74	catgacggcccgaggcggt	60	19
107772	Coding	3	113	ccggacttgtcgatctgt	95	20
107773	Coding	3	154	ctggcttcatgtcggtatc	88	21
107774	Coding	3	178	tggccactctacatggaa	77	22
107775	Coding	3	223	ggactgacgtctctgtacct	75	23
107776	Coding	3	252	gaatgtttttatccgacta	82	24
107777	Coding	3	280	ctagcgttgtatagtattt	29	25
107778	Coding	3	324	gggttaagaatgttaactcc	86	26
107779	Coding	3	352	tgaccgcatttgtttaggcaa	75	27
107780	Coding	3	381	ttttctgtcccacaccatc	30	28
107781	Coding	3	408	ctctgttgcgttgcacgaca	78	29
107782	Coding	3	436	gcgcattttaaacgaaacctt	83	30
107783	Coding	3	490	aaattttgttgtttcaaaagat	0	31
107784	Coding	3	519	tgtatatcttcagagatcaat	57	32
107785	Coding	3	547	tcttagctgtcgacttgtata	74	33

- 68 -

	107786	Coding	3	575	agtttccttgggttttaagg	33	34
5	107787	Coding	3	604	gtggatatagtggaaaatgtaa	51	35
	107788	Coding	3	632	tgtttcaggcacccaaagt	55	36
	107789	Coding	3	661	ttagaaaaagaaaatgtcaagaa	17	37
	107790	Coding	3	688	gggtcgatgtacccgtactc	61	38
10	107791	Coding	3	716	gcagtgcaccacaacggcc	81	39
	107792	Coding	3	744	aggttccagacacctgcccgt	81	40
	107793	Coding	3	772	agcaggaggcaggatgtcagc	2	41
	107794	Coding	3	799	gaagaagggtttttcccttt	53	42
15	107795	Coding	3	826	tctaacagcacttcttgat	18	43
	107796	Coding	3	853	atcaaccccatcgcggaaactt	0	44
	107797	Coding	3	880	gagaagcgcagtcgtcgcc	82	45
	107798	Coding	3	908	tttgcacccatcgatcacag	62	46
	107799	Coding	3	952	agctcccttccactgtatctg	70	47
20	107800	Coding	3	1024	tccaggatcgttttgg	72	48
	107801	Coding	3	1052	gaactccctgcatttccat	68	49
	107802	Coding	3	1079	ttcccttcacccactgggtgt	40	50
	107803	Coding	3	1148	gttagggtcggcatttaaagg	0	51
	107804	Coding	3	1176	cagtgttgcgtactatgttt	75	52
25	107805	Coding	3	1222	gcctgggcacccgtcgaaact	67	53
	107806	Coding	3	1268	ctcgcccttcgtggcgtgt	37	54
	107807	Coding	3	1295	gggtttccaggtaactcgtgt	73	55
	107808	Coding	3	1323	ccgttagccacgcacatgtt	80	56
	107809	Coding	3	1351	tagcagaggtaaaggcggc	72	57
30	107810	Stop Codon	3	1379	ctatgttgtgttgttgcaca	85	58
	107811	3' UTR	3	1404	ggagggtggatgggggggg	51	59
	107812	3' UTR	3	1433	ggctctggggcagaggcg	81	60
	107813	3' UTR	3	1460	ccgcggcatgcgtctgtc	84	61
	107814	3' UTR	3	1489	tctctacgcgttccggcggc	84	62
35	107815	3' UTR	3	1533	aagatgggttttttgtcaga	65	63
	107816	3' UTR	3	1634	gtactcttcactctct	69	64
	107817	3' UTR	3	1662	ggccccctcccttcgtcgccg	59	65
	107818	3' UTR	3	1707	ctccaggggggggccctgg	57	66
	107819	3' UTR	3	1735	gggttgtggcggtgcgcgc	54	67
40	107820	3' UTR	3	1783	tttaaaataaaatgtgttgt	0	68
	107821	3' UTR	3	1831	gttcaagaaaatgtgttgtc	69	69
	107822	3' UTR	3	1884	ttggataaaaggccctgtgtca	74	70
	107823	3' UTR	3	1936	atggcaaaaggcccttcattcc	26	71
	107824	3' UTR	3	1973	gtcctcttcaggactactgg	60	72
45	107825	3' UTR	3	2011	ttacccacaatatactaaaa	39	73
	107826	3' UTR	3	2045	attatataattatgtgttgt	24	74
	107827	3' UTR	3	2080	tcacatcatgtttttatata	48	75
	107828	3' UTR	3	2115	ataacaggggggagaataag	0	76
	107829	3' UTR	3	2170	ttacatgtttttatatacac	21	77
	107830	3' UTR	3	2223	gatcaaaggtttttttttttt	81	78
	107831	3' UTR	3	2274	ggtcgtgcacaggcagggtt	82	79
	107832	3' UTR	3	2309	caacaggctttaggaaccaca	65	80

- 69 -

	107833	3' UTR	3	2344	aactgcaccctatgtcgag	61	81
	107834	3' UTR	3	2380	gtcatgccageaaattagcaa	0	82
5	107835	3' UTR	3	2413	acaggctgggcctcacagg	58	83
	107836	3' UTR	3	2443	ttagthacagcaagaccctg	44	84
	107837	3' UTR	3	2473	gaataatggttccatcaccc	0	85
	107838	3' UTR	3	2502	ccctaaatcatgtccagagc	87	86
10	107839	3' UTR	3	2558	gacttggaaatggcgaggct	74	87
	107840	3' UTR	3	2587	caaatcacegttgctcaag	31	88
	107841	3' UTR	3	2618	gaagtgtgggttccagcagg	56	89
15	107842	3' UTR	3	2648	ccttaaggaccgtcacccag	42	90
	107843	3' UTR	3	2678	gtgaaccgggacagagacgg	25	91
	107844	3' UTR	3	2724	gccccacaggggttgtgggt	53	92
	107845	3' UTR	3	2755	cctttgccggaaatgtggagg	75	93
	107846	3' UTR	3	2785	aaagccacttaatgtggagg	79	94
	107847	3' UTR	3	2844	gtgaaaatgtggcaagaga	86	95
	107848	3' UTR	3	2970	tcaagaatgtttacagccctgg	61	96

As shown in Table 1, SEQ ID NOs 18, 19, 20, 21, 22, 23, 24, 26, 27, 29, 30, 32, 33, 35, 36, 38, 39, 40, 42, 45, 46, 47, 48, 49, 50, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 69, 70, 72, 73, 75, 78, 79, 80, 81, 83, 84, 86, 87, 89, 90, 92, 93, 94, 95, and 96 demonstrated at least 35% inhibition of human PTP1B expression in this assay and are therefore preferred.

Example 16

Antisense inhibition of rat PTP1B expression by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap.

In accordance with the present invention, a second series of oligonucleotides were designed to target different regions of the rat PTP1B RNA, using published sequences (GenBank accession number M33962, incorporated herein as SEQ ID NO: 10). The oligonucleotides are shown in Table 2. "Target site" indicates the first (5'-most) nucleotide number on the particular target sequence to which the oligonucleotide binds. All compounds in Table 2 are chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings". The wings are composed of 2'-methoxyethyl (2'-MOE)nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the

- 70 -

oligonucleotide. All cytidine residues are 5-methylcytidines. The compounds were analyzed for their effect on rat PTP1B mRNA levels by quantitative real-time PCR as described in other examples herein. Data are averages from two experiments. If present, "N.D." indicates "no data".

5

Table 2

Inhibition of rat PTP1B mRNA levels by chimeric phosphorothioate oligonucleotides
having 2'-MOE wings and a deoxy gap

	ISIS #	REGION	TARGET SEQ ID NO	TARGET SITE	SEQUENCE	% INHIB	SEQ ID NO
10	111549	5' UTR	10	1	caaccctcccagcagcggct	32	97
	111550	5' UTR	10	33	tgcaggcccgtcgcggcca	27	98
	111551	5' UTR	10	73	cctcgccgtccgcgcgt	34	99
	111552	Coding	10	132	tgcgtctgcgtcaattccctt	49	100
	113669	Coding	10	164	cctggtaaatagccggccag	36	101
15	113670	Coding	10	174	tgtcgaaatatccgttaaat	63	102
	113671	Coding	10	184	actggcgtcatgtcgaaatat	58	103
	113672	Coding	10	189	aagtcaactggcttcatgtcg	40	104
	111553	Coding	10	190	gaagtcactggcttcatgtc	27	105
	113673	Coding	10	191	ggaagtcaactggcttcatgt	54	106
20	113674	Coding	10	192	gaaaagtcaactggcttcatg	41	107
	113675	Coding	10	193	tggaaagtcaactggcttcat	56	108
	113676	Coding	10	194	atggaaagtcaactggctca	31	109
	113677	Coding	10	195	cataggaaagtcaactggcttc	59	110
	113678	Coding	10	225	ttttgtctttagaagttt	24	111
25	111554	Coding	10	228	cgttttttgttttagaag	45	112
	111555	Coding	10	269	tccgactgttgtcaaaaagg	39	113
	113679	Coding	10	273	ttaatccgactgttgtcaaa	45	114
	113680	Coding	10	298	atagtcattatctccctgtat	49	115
	111556	Coding	10	303	ttgatatagtcaattatcttc	29	116
30	113681	Coding	10	330	gcttcctccatttttatcaa	67	117
	111557	Coding	10	359	ggccctgggtggatataatag	20	118
	113682	Coding	10	399	cacaccatctcccaagaagt	29	119
	111558	Coding	10	405	tgctccccacacatctccca	48	120
	113683	Coding	10	406	ctgctccccacacatctccc	51	121
35	113684	Coding	10	407	tctgtccccacacatctcc	37	122
	113685	Coding	10	408	ttctgtccccacacatcttc	54	123
	113686	Coding	10	417	ccccctgtcttcgtccccca	60	124
	111559	Coding	10	438	atgcgttgtggatgaccac	15	125
	113687	Coding	10	459	ttaacgagcccttctccat	33	126

- 71 -

	113688	Coding	10	492	ttttcttcttcgtggcca	54	127
	113689	Coding	10	502	gaccatctctttttttttt	58	128
5	111560	Coding	10	540	tcaagagatcagtgtcagtt	21	129
	113690	Coding	10	550	cttgacatcttcagagatca	64	130
	113691	Coding	10	558	taatatgtacttgacatttc	46	131
	111561	Coding	10	579	aactccaaactgcccgtactgt	14	132
10	111562	Coding	10	611	tcttcgaggctctgggta	38	133
	113692	Coding	10	648	ccaaaggcaggccagggttgt	63	134
	111563	Coding	10	654	ggpactccaaaggcaggcca	31	135
15	113693	Coding	10	655	aggggactccaaaggtcaggcc	50	136
	113694	Coding	10	656	caggggactccaaaggtcaggc	45	137
	113695	Coding	10	657	tcaagggactccaaaggtcagg	49	138
	113696	Coding	10	663	ggtgactcaggggactccaaa	34	139
20	111564	Coding	10	705	cctgactctcgacttttggaa	53	140
	113697	Coding	10	715	gctgggtggccgtgactctc	57	141
	113698	Coding	10	726	ccgtgcctctgggtggatgtga	48	142
	111565	Coding	10	774	aagggtccctgacactgccaat	28	143
	111566	Coding	10	819	tctttcccttgcgtccatcg	34	144
25	113699	Coding	10	820	gtctttcccttgcgtccatca	41	145
	113700	Coding	10	821	ggctttcccttgcgtccatc	66	146
	113701	Coding	10	822	gggtcttcccttgcgtccat	71	147
	113702	Coding	10	852	aacagcacccgttgcgtatgc	39	148
	111567	Coding	10	869	ggaacctgcgcacatccaaac	0	149
	111568	Coding	10	897	tggtggccgtctggatgag	29	150
30	113703	Coding	10	909	gagaaggcgcgttgtgcggc	48	151
	113704	Coding	10	915	aggtaggagaagccgcgcgtg	31	152
	113705	Coding	10	918	gccacggtaaggagaagcgcgc	41	153
	111569	Coding	10	919	agccaggttaggagaagcgc	56	154
	113706	Coding	10	920	cagccaggtagggagaagcgc	58	155
35	113707	Coding	10	921	acagccaggtagggagaagcg	43	156
	113708	Coding	10	922	cacagccaggtagggagaagc	49	157
	113709	Coding	10	923	tcacagccaggtagggagaag	47	158
	111570	Coding	10	924	atcacagccaggtagggaga	51	159
40	113710	Coding	10	925	gatcacagccaggtagggaga	51	160
	113711	Coding	10	926	cgatcacagccaggtagggag	63	161
	113712	Coding	10	927	tgcatcacagccaggtaggg	71	162
	113713	Coding	10	932	caccctgtatccacagccagg	75	163
	113714	Coding	10	978	tccctccactgtatctgcac	97	164
45	111571	Coding	10	979	cicccitccactgtatctgc	89	165
	113715	Coding	10	980	gtccctccactgtatctgc	99	166
	107799	Coding	10	981	agctcttccactgtatctg	99	167
	113716	Coding	10	982	aagctcttccactgtatct	97	168
	113717	Coding	10	983	aaagctcttccactgtatcc	95	169
	113718	Coding	10	984	gaaagctcttccactgtatc	95	170
	113719	Coding	10	985	ggaaagctcttccactgtat	95	171
	111572	Coding	10	986	ggggaaagctcttccactgt	89	172
	113720	Coding	10	987	ttggggaaagctcttccactgt	97	173
	113721	Coding	10	1036	tggccggggpaggtggggca	20	174

- 72 -

	111573	Coding	10	1040	tgggtggccggggagggtggg	20	175
	113722	Coding	10	1046	tgcgttgggtggccggga	18	176
5	111574	Coding	10	1073	tgcacttcattgttaggc	38	177
	113723	Coding	10	1206	acitcagtgtcttgactcat	67	178
	113724	Coding	10	1207	aacticatgtcttgactca	60	179
10	111575	Coding	10	1208	taacticatgtcttgactc	50	180
	113725	Coding	10	1209	ctaacticatgtcttgact	53	181
	111576	Coding	10	1255	gacagatgccatggacactt	32	182
	106409	Coding	10	1333	gaccaggaaagggttcagg	32	183
15	113726	Coding	10	1334	tgaccaggaaagggttcagg	39	184
	111577	Coding	10	1335	ttgaccaggaaagggttcagg	32	185
	113727	Coding	10	1336	gttgaccaggaaagggttcagg	41	186
	113728	Coding	10	1342	gcacacgttgaccaggaaagg	59	187
20	111578	Coding	10	1375	gaggtagcgccatgtgcga	45	188
	111579	Coding	10	1387	taccctggtaacagaggtag	32	189
	111580	Coding	10	1397	agtgtaaaacatacccgtaa	30	190
	111581	3' UTR	10	1456	caaatccataacctggcagt	31	191
	111582	3' UTR	10	1519	ttccagttccaccacaggct	24	192
25	111583	3' UTR	10	1552	ccagtgacagatgtccccctc	47	193
	111584	3' UTR	10	1609	acagggttaaggccctgtggat	29	194
	111585	3' UTR	10	1783	gccttagcatacttttgttgc	43	195
	111586	3' UTR	10	1890	aaggccagcaggaaactttaca	36	196
	111587	3' UTR	10	2002	ggggcacccctggggaaaggcag	16	197
	111588	3' UTR	10	2048	ggtcatctgcaagatggcgg	40	198
30	111589	3' UTR	10	2118	gcacccatctgtatggaccctg	25	199
	111590	3' UTR	10	2143	tggaaaggcccaggctctaa	25	200
	111591	3' UTR	10	2165	tagtaatgactttcaatca	44	201
	111592	3' UTR	10	2208	ttagtcttgccttacacctc	41	202
	111593	3' UTR	10	2252	cctgcgcggagtgacttc	22	203
35	111594	3' UTR	10	2299	aggacgttactgtcgacggaa	43	204
	111595	3' UTR	10	2346	tcaggacaatgtttggcagt	32	205
	111596	3' UTR	10	2405	gaggctgtcacatgtggcgt	34	206
	111597	3' UTR	10	2422	tcatgttttttttttttttttt	20	207
	111598	3' UTR	10	2449	accacatgttttttttttttt	30	208
40	111599	3' UTR	10	2502	atgtgggttttttttttttttt	30	209
	111600	3' UTR	10	2553	cagctgttttttttttttttt	8	210
	111601	3' UTR	10	2608	aggaaagggttttttttttttt	32	211
	111602	3' UTR	10	2664	cccttcacgttttttttttttt	24	212
	111603	3' UTR	10	2756	catttttttttttttttttttt	18	213
45	111604	3' UTR	10	2830	caggctgttttttttttttttt	30	214
	111605	3' UTR	10	2883	gtcttacacttcaacccttagg	37	215
	111606	3' UTR	10	2917	ctggcccccaggccaccagccaca	12	216
	111607	3' UTR	10	2946	atgttttttttttttttttttt	33	217
	111608	3' UTR	10	2978	ttagatgttttttttttttttt	28	218
	111609	3' UTR	10	3007	tacatgttttttttttttttt	37	219
	111610	3' UTR	10	3080	tttttttttttttttttttttt	30	220
	111611	3' UTR	10	3153	gtggcccccagggtggcggc	23	221
	111612	3' UTR	10	3206	cggttttttttttttttttttt	27	222

- 73 -

	111613	3' UTR	10	3277	gtggaaatgtctgagatccag	31	223
	111614	3' UTR	10	3322	aggcccgggcctgttgtccca	23	224
	111615	3' UTR	10	3384	cggttccctggccctgtcccaga	31	225
	111616	3' UTR	10	3428	tacactgttcccaggagggt	42	226
5	111617	3' UTR	10	3471	tggtgccagcagcgcttagca	10	227
	111618	3' UTR	10	3516	cagtcttcagcgtcaaga	43	228
	113729	3' UTR	10	3537	aagagtcatgagcaccatca	56	229
	111619	3' UTR	10	3560	tgaaggtacaagtccccctca	40	230
10	111620	3' UTR	10	3622	ctggcaagaggcagactgga	30	231
	111621	3' UTR	10	3666	ggctctgtgtgttgtttct	52	232
	111622	3' UTR	10	3711	gccatcttcicagcctgtgc	39	233
	111623	3' UTR	10	3787	agcgcctgtgtgtggggcccc	16	234
	111624	3' UTR	10	3854	tgtgtgtgttgttgttgtt	35	235
15	111625	3' UTR	10	3927	ctatggccattttagagagag	36	236
	113730	3' UTR	10	3936	tggttttttttttatggccatt	59	237
	111626	3' UTR	10	3994	cgtccctgtcaaaagggtgttat	11	238
	111627	3' UTR	10	4053	gttggaaaacggtgcatgtcg	39	239
	111628	3' UTR	10	4095	atttatgtgtcaactaatg	33	240

As shown in Table 2, SEQ ID NOs 97, 99, 100, 101, 102, 103, 104, 106, 107,
20 108, 109, 110, 112, 113, 114, 115, 117, 120, 121, 122, 123, 124, 126, 127, 128, 130,
131, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 144, 145, 146, 147, 148, 151,
152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168,
169, 170, 171, 172, 173, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188,
189, 191, 193, 195, 196, 198, 201, 202, 204, 205, 206, 211, 215, 217, 219, 223, 225,
25 226, 228, 229, 230, 232, 233, 235, 236, 237, 239 and 240 demonstrated at least 30%
inhibition of rat PTP1B expression in this experiment and are therefore preferred.

Example 17

Western blot analysis of PTP1B protein levels

Western blot analysis (immunoblot analysis) is carried out using standard
30 methods. Cells are harvested 16-20 h after oligonucleotide treatment, washed once
with PBS, suspended in Laemmli buffer (100 μ l/well), boiled for 5 minutes and loaded
on a 16% SDS-PAGE gel. Gels are run for 1.5 hours at 150 V, and transferred to
membrane for western blotting. Appropriate primary antibody directed to PTP1B is
used, with a radiolabelled or fluorescently labeled secondary antibody directed against

- 74 -

the primary antibody species. Bands are visualized using a PHOSPHORIMAGER™ (Molecular Dynamics, Sunnyvale CA).

Example 18

Effects of antisense inhibition of PTP1B (ISIS 113715) on blood glucose levels

5 db/db mice are used as a model of Type 2 diabetes. These mice are hyperglycemic, obese, hyperlipidemic, and insulin resistant. The db/db phenotype is due to a mutation in the leptin receptor on a C57BLKS background. However, a mutation in the leptin gene on a different mouse background can produce obesity without diabetes (ob/ob mice). Leptin is a hormone produced by fat that regulates 10 appetite and animals or humans with leptin deficiencies become obese. Heterozygous db/wt mice (known as lean littermates) do not display the hyperglycemia/hyperlipidemia or obesity phenotype and are used as controls.

In accordance with the present invention, ISIS 113715 (GCTCCTTCCACTGATCCTGC, SEQ ID No: 166) was investigated in experiments 15 designed to address the role of PTP1B in glucose metabolism and homeostasis. ISIS 113715 is completely complementary to sequences in the coding region of the human, rat, and mouse PTP1B nucleotide sequences incorporated herein as SEQ ID No: 3 (starting at nucleotide 951 of human PTP1B; Genbank Accession No. M31724), SEQ ID No: 10 (starting at nucleotide 980 of rat PTP1B; Genbank Accession No. M33962) and SEQ ID No: 241 (starting at nucleotide 1570 of mouse PTP1B; Genbank 20 Accession No. U24700). The control used is ISIS 29848 (NNNNNNNNNNNNNNNNNN, SEQ ID No: 242) where N is a mixture of A, G, T and C.

Male db/db mice and lean (heterozygous, i.e., db/wt) littermates (age 9 weeks at 25 time 0) were divided into matched groups (n=6) with the same average blood glucose levels and treated by intraperitoneal injection once a week with saline, ISIS 29848 (the control oligonucleotide) or ISIS 113715. db/db mice were treated at a dose of 10, 25 or 50 mg/kg of ISIS 113715 or 50 mg/kg of ISIS 29848 while lean littermates were treated at a dose of 50 or 100 mg/kg of ISIS 113715 or 100 mg/kg of ISIS 29848.

- 75 -

Treatment was continued for 4 weeks with blood glucose levels being measured on day 0, 7, 14, 21 and 28.

By day 28 in db/db mice, blood glucose levels were reduced at all doses from a starting level of 300 mg/dL to 225 mg/dL for the 10 mg/kg dose, 175 mg/dL for the 25 mg/kg dose and 125 mg/dL for the 50 mg/kg dose. These final levels are within normal range for wild-type mice (170 mg/dL). The mismatch control and saline treated levels 5 were 320 mg/dL and 370 mg/dL at day 28, respectively.

In lean littermates, blood glucose levels remained constant throughout the study for all treatment groups (average 120 mg/dL). These results indicate that treatment 10 with ISIS 113715 reduces blood glucose in db/db mice and that there is no hypoglycemia induced in the db/db or the lean littermate mice as a result of the oligonucleotide treatment.

In a similar experiment, ob/ob mice and their lean littermates (heterozygous, i.e., ob/wt) were dosed twice a week at 50 mg/kg with ISIS 113715, ISIS 29848 or 15 saline control and blood glucose levels were measured at the end of day 7, 14 and 21. Treatment of ob/ob mice with ISIS 113715 resulted in the largest decrease in blood glucose over time going from 225 mg/dL at day 7 to 95 mg/dL at day 21. Ob/ob mice displayed an increase in plasma glucose over time from 300 mg/dL to 325 mg/dL while treatment with the control oligonucleotide reduced plasma glucose from an average of 20 280 mg/dL to 130 mg/dL. In the lean littermates plasma glucose levels remained unchanged in all treatment groups (average level 100 mg/dL).

Example 19

Effects of antisense inhibition of PTP1B (ISIS 113715) on mRNA expression in liver

25 Male db/db mice and lean littermates (age 9 weeks at time 0) were divided into matched groups (n=6) with the same average blood glucose levels and treated by intraperitoneal injection once a week with saline, ISIS 29848 (the control oligonucleotide) or ISIS 113715. db/db mice were treated at a dose of 10, 25 or 50 mg/kg of ISIS 113715 or 50 mg/kg of ISIS 29848 while lean littermates were treated

- 76 -

at a dose of 50 or 100 mg/kg of ISIS 113715 or 100 mg/kg of ISIS 29848. Treatment was continued for 4 weeks after which the mice were sacrificed and tissues collected for mRNA analysis. RNA values were normalized and are expressed as a percentage of saline treated control.

5 ISIS 113715 successfully reduced PTP1B mRNA levels in the livers of db/db mice at all doses examined (60% reduction of PTP1B mRNA), whereas the control oligonucleotide treated animals showed no reduction in PTP1B mRNA, remaining at the level of the saline treated control. Treatment of lean littermates with ISIS 113715 also reduced mRNA levels to 45% of control at the 50 mg/kg dose and 25% of control
10 at the 100 mg/kg dose. The control oligonucleotide (ISIS 29848) failed to show any reduction in mRNA levels.

Example 20

Effects of antisense inhibition of PTP1B (ISIS 113715) on body weight

Male db/db mice and lean littermates (age 9 weeks at time 0) were divided into
15 matched groups (n=6) with the same average blood glucose levels and treated by intraperitoneal injection once a week with saline, ISIS 29848 (the control oligonucleotide) or ISIS 113715. db/db mice were treated at a dose of 10, 25 or 50 mg/kg of ISIS 113715 or 50 mg/kg of ISIS 29848 while lean littermates were treated at a dose of 50 or 100 mg/kg of ISIS 113715 or 100 mg/kg of ISIS 29848. Treatment
20 was continued for 4 weeks. At day 28 mice were sacrificed and final body weights were measured.

Treatment of ob/ob mice with ISIS 113715 resulted in an increase in body weight which was constant over the dose range with animals gaining an average of 11.0 grams while saline treated controls gained 5.5 grams. Animals treated with the control oligonucleotide gained an average of 7.8 grams of body weight.
25

Lean littermate animals treated with 50 or 100 mg/kg of ISIS 113715 gained 3.8 grams of body weight compared to a gain of 3.0 grams for the saline controls.

- 77 -

In a similar experiment, ob/ob mice and their lean littermates were dosed twice a week at 50 mg/kg with ISIS 113715, ISIS 29848 or saline control and body weights were measured at the end of day 7, 14 and 21.

Treatment of the ob/ob mice with ISIS 113715, ISIS 29848 or saline control all resulted in a similar increase in body weight across the 21-day timecourse. At the end of day 7 all ob/ob treatment groups had an average weight of 42 grams. By day 21, animals treated with ISIS 113715 had an average body weight of 48 grams, while those in the ISIS 29848 (control oligonucleotide) and saline control group each had an average body weight of 52 grams. All of the lean littermates had an average body weight of 25 grams at the beginning of the timecourse and all lean littermate treatment groups showed an increase in body weight, to 28 grams, by day 21.

Example 21

Effects of antisense inhibition of PTP1B (ISIS 113715) on plasma insulin levels

Male db/db mice (age 9 weeks at time 0) were divided into matched groups (n=6) with the same average blood glucose levels and treated by intraperitoneal injection twice a week with saline, ISIS 29848 (the control oligonucleotide) or ISIS 113715 at a dose of 50 mg/kg. Treatment was continued for 3 weeks with plasma insulin levels being measured on day 7, 14, and 21.

Mice treated with ISIS 113715 showed a decrease in plasma insulin levels from 15 ng/mL at day 7 to 7.5 ng/mL on day 21. Saline treated animals has plasma insulin levels of 37 ng/mL at day 7 which dropped to 25 ng/mL on day 14 but rose again to 33 ng/mL by day 21. Mice treated with the control oligonucleotide also showed a decrease in plasma insulin levels across the timecourse of the study from 25 ng/mL at day 7 to 10 ng/mL on day 21. However, ISIS 113715 was the most effective at reducing plasma insulin over time.

- 78 -

What is claimed is:

1. A compound 8 to 50 nucleobases in length targeted to a nucleic acid molecule encoding PTP1B, wherein said compound specifically hybridizes with and inhibits the expression of PTP1B.
2. The compound of claim 1 which is an antisense oligonucleotide.
3. The compound of claim 2 wherein the antisense oligonucleotide has a sequence comprising SEQ ID NO: 18, 19, 20, 21, 22, 23, 24, 26, 27, 29, 30, 32, 33, 35, 36, 38, 39, 40, 42, 45, 46, 47, 48, 49, 50, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 69, 70, 72, 73, 75, 78, 79, 80, 81, 83, 84, 86, 87, 89, 90, 92, 93, 94, 95, 96, 97, 99, 100, 101, 102, 103, 104, 106, 107, 108, 109, 110, 112, 113, 114, 115, 117, 120, 121, 122, 123, 124, 126, 127, 128, 130, 131, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 144, 145, 146, 147, 148, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 168, 169, 170, 171, 172, 173, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 191, 193, 195, 196, 198, 201, 202, 204, 205, 206, 211, 215, 217, 219, 223, 225, 226, 228, 229, 230, 232, 233, 235, 236, 237, 239 or 240.
4. The compound of claim 2 wherein the antisense oligonucleotide comprises at least one modified internucleoside linkage.
5. The compound of claim 4 wherein the modified internucleoside linkage is a phosphorothioate linkage.
6. The compound of claim 2 wherein the antisense oligonucleotide comprises at least one modified sugar moiety.

- 79 -

7. The compound of claim 6 wherein the modified sugar moiety is a 2'-O-methoxyethyl sugar moiety.

8. The compound of claim 2 wherein the antisense oligonucleotide comprises at least one modified nucleobase.

9. The compound of claim 8 wherein the modified nucleobase is a 5-methylcytosine.

10. The compound of claim 2 wherein the antisense oligonucleotide is a chimeric oligonucleotide.

11. A composition comprising the compound of claim 1 and a pharmaceutically acceptable carrier or diluent.

12. The composition of claim 11 further comprising a colloidal dispersion system.

13. The composition of claim 11 wherein the compound is an antisense oligonucleotide.

14. A compound 8 to 50 nucleobases in length which specifically hybridizes with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding PTP1B.

15. A method of inhibiting the expression of PTP1B in cells or tissues comprising contacting said cells or tissues with the compound of claim 1 so that expression of PTP1B is inhibited.

- 80 -

16. The method of claim 15 wherein the cells or tissues are human cells or tissues.
17. The method of claim 15 wherein the cells or tissues are rodent cells or tissues.
18. The method of claim 17 wherein the rodent cells or tissues are mouse cells or tissues.
19. The method of claim 17 wherein the rodent cells or tissues are rat cells or tissues.
20. The method of claim 15 wherein the cells or tissues are liver, kidney or adipose cells or tissues.
21. A method of treating an animal having or suspected of having a disease or condition associated with PTP1B comprising administering to said animal a therapeutically or prophylactically effective amount of the compound of claim 1 so that expression of PTP1B is inhibited.
22. The method of claim 21 wherein the animal is a human.
23. The method of claim 21 wherein the disease or condition is a metabolic disease or condition.
24. The method of claim 21 wherein the disease or condition is diabetes.
25. The method of claim 21 wherein the disease or condition is Type 2 diabetes.

- 81 -

26. The method of claim 21 wherein the disease or condition is obesity.
27. The method of claim 21 wherein the disease or condition is a hyperproliferative condition.
28. The method of claim 27 wherein the hyperproliferative condition is cancer.
29. A method of decreasing blood glucose levels in an animal comprising administering to said animal the compound of claim 1.
30. The method of claim 29 wherein the animal is a human or a rodent.
31. The method of claim 29 wherein the blood glucose levels are plasma glucose levels or serum glucose levels.
32. The method of claim 29 wherein the animal is a diabetic animal.
33. A method of preventing or delaying the onset of a disease or condition associated with PTP1B in an animal comprising administering to said animal a therapeutically or prophylactically effective amount of the compound of claim 1.
34. The method of claim 33 wherein the animal is a human.
35. The method of claim 33 wherein the disease or condition is a metabolic disease or condition.
36. The method of claim 33 wherein the disease or condition is diabetes.

- 82 -

37. The method of claim 33 wherein the disease or condition is Type 2 diabetes.
38. The method of claim 33 wherein the disease or condition is obesity.
39. The method of claim 33 wherein the disease or condition is a hyperproliferative condition.
40. The method of claim 39 wherein the hyperproliferative condition is cancer.
41. A method of preventing or delaying the onset of an increase in blood glucose levels in an animal comprising administering to said animal the compound of claim 1.
42. The method of claim 41 wherein the animal is a human or a rodent.
43. The method of claim 41 wherein the blood glucose levels are plasma glucose levels or serum glucose levels.
44. The method of claim 41 wherein the animal is a diabetic animal.

SEQUENCE LISTING

<110> Lex M. Cowser
Jacqueline Wyatt
Susan M. Freier
Brett P. Monia
Madeline M. Butler
Robert McKay

<120> ANTISENSE MODULATION OF PTP1B EXPRESSION

<130> ISPH-0478

<140> US 09/629,644
<141> 2000-07-31

<150> US 09/487,368
<151> 2000-01-18

<160> 242

<210> 1
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 1
tccgtcatcg ctcctcaggg

20

<210> 2
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 2
atgcattctg cccccaagga

20

<210> 3
<211> 3247
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (91)...(1398)

<400> 3
gggcgggcct cggggctaag agcgcgacgc ctagagcggc agacggcgca gtggggcgag 60
aaggaggcgcc agcagccgcc ctggcccgtc atg gag atg gaa aag gag ttc gag 114
Met Glu Met Glu Lys Glu Phe Glu

1	5	
cag atc gac aag tcc ggg agc tgg gcg gcc att tac cag gat atc cga Gln Ile Asp Lys Ser Gly Ser Trp Ala Ala Ile Tyr Gln Asp Ile Arg 10 15 20		162
cat gaa gcc agt gac ttc cca tgt aga gtg gcc aag ctt cct aag aac His Glu Ala Ser Asp Phe Pro Cys Arg Val Ala Lys Leu Pro Lys Asn 25 30 35 40		210
aaa aac cga aat agg tac aga gac gtc agt ccc ttt gac cat agt cgg Lys Asn Arg Asn Arg Tyr Arg Asp Val Ser Pro Phe Asp His Ser Arg 45 50 55		258
att aaa cta cat caa gaa gat aat gac tat atc aac gct agt ttg ata Ile Lys Leu His Gln Glu Asp Asn Asp Tyr Ile Asn Ala Ser Leu Ile 60 65 70		306
aaa atg gaa gaa gcc caa agg agt tac att ctt acc cag ggc cct ttg Lys Met Glu Glu Ala Gln Arg Ser Tyr Ile Leu Thr Gln Gly Pro Leu 75 80 85		354
cct aac aca tgc ggt cac ttt tgg gag atg gtg tgg gag cag aaa agc Pro Asn Thr Cys Gly His Phe Trp Glu Met Val Trp Glu Gln Lys Ser 90 95 100		402
agg ggt gtc gtc atg ctc aac aga gtg atg gag aaa ggt tcg tta aaa Arg Gly Val Val Met Leu Asn Arg Val Met Glu Lys Gly Ser Leu Lys 105 110 115 120		450
tgc gca caa tac tgg cca caa aaa gaa gaa aaa gag atg atc ttt gaa Cys Ala Gln Tyr Trp Pro Gln Lys Glu Glu Lys Glu Met Ile Phe Glu 125 130 135		498
gac aca aat ttg aaa tta aca ttg atc tot gaa gat atc aag tca tat Asp Thr Asn Leu Lys Leu Thr Leu Ile Ser Glu Asp Ile Lys Ser Tyr 140 145 150		546
tat aca gtg cga cag cta gaa ttg gaa aac ctt aca acc caa gaa act Tyr Thr Val Arg Gln Leu Glu Leu Asn Leu Thr Thr Gln Glu Thr 155 160 165		594
cga gag atc tta cat ttc cac tat acc aca tgg cct gac ttt gga gtc Arg Glu Ile Leu His Phe His Tyr Thr Trp Pro Asp Phe Gly Val 170 175 180		642
cct gaa tca cca gcc tca ttc ttg aac ttt ctt ttc aaa gtc cga gag Pro Glu Ser Pro Ala Ser Phe Leu Asn Phe Leu Phe Lys Val Arg Glu 185 190 195 200		690
tca ggg tca ctc agc ccg gag cac ggg ccc gtt gtg gtg cac tgc agt Ser Gly Ser Leu Ser Pro Glu His Gly Pro Val Val His Cys Ser 205 210 215		738
gca ggc atc ggc agg tct gga acc ttc tgt ctg gct gat acc tgc ctc Ala Gly Ile Gly Arg Ser Gly Thr Phe Cys Leu Ala Asp Thr Cys Leu 220 225 230		786
ctg ctg atg gac aag agg aaa gac cct tct tcc gtt gat atc aag aaa		834

Leu Leu Met Asp Lys Arg Lys Asp Pro Ser Ser Val Asp Ile Lys Lys			
235	240	245	
gtg ctg tta gaa atg agg aag ttt cgg atg ggg ttg atc cag aca gcc			882
Val Leu Leu Glu Met Arg Lys Phe Arg Met Gly Leu Ile Gln Thr Ala			
250	255	260	
gac cag ctg cgc ttc tcc tac ctg gct gtg atc gaa ggt gcc aaa ttc			930
Asp Gln Leu Arg Phe Ser Tyr Leu Ala Val Ile Glu Gly Ala Lys Phe			
265	270	275	280
atc atg ggg gac tct tcc gtg cag gat cag tgg aag gag ctt tcc cac			978
Ile Met Gly Asp Ser Ser Val Gln Asp Gln Trp Lys Glu Leu Ser His			
285	290	295	
gag gac ctg gag ccc cca ccc gag cat atc ccc cca cct ccc cgg cca			1026
Glu Asp Leu Glu Pro Pro Pro Glu His Ile Pro Pro Pro Pro Arg Pro			
300	305	310	
ccc aaa cga atc ctg gag cca cac aat ggg aaa tgc agg gag ttc ttc			1074
Pro Lys Arg Ile Leu Glu Pro His Asn Gly Lys Cys Arg Glu Phe Phe			
315	320	325	
cca aat cac cag tgg gtg aag gaa gag acc cag gag gat aaa gac tgc			1122
Pro Asn His Gln Trp Val Lys Glu Glu Thr Gln Glu Asp Lys Asp Cys			
330	335	340	
ccc atc aag gaa gaa aaa gga agc ccc tta aat gcc gca ccc tac ggc			1170
Pro Ile Lys Glu Glu Lys Gly Ser Pro Leu Asn Ala Ala Pro Tyr Gly			
345	350	355	360
atc gaa agc atg agt caa gac act gaa gtt aga agt cgg gtc gtg ggg			1218
Ile Glu Ser Met Ser Gln Asp Thr Glu Val Arg Ser Arg Val Val Gly			
365	370	375	
gga agt ctt cga ggt gcc cag gct gcc tcc cca gcc aaa ggg gag ccg			1266
Gly Ser Leu Arg Gly Ala Gln Ala Ala Ser Pro Ala Lys Gly Glu Pro			
380	385	390	
tca ctg ccc gag aag gac gag gac cat gca ctg agt tac tgg aag ccc			1314
Ser Leu Pro Glu Lys Asp Glu Asp His Ala Leu Ser Tyr Trp Lys Pro			
395	400	405	
ttc ctg gtc aac atg tgc gtg gct acg gtc ctc acg gcc ggc gct tac			1362
Phe Leu Val Asn Met Cys Val Ala Thr Val Leu Thr Ala Gly Ala Tyr			
410	415	420	
ctc tgc tac agg ttc ctg ttc aac agc aac aca tag cctgaccctc			1408
Leu Cys Tyr Arg Phe Leu Phe Asn Ser Asn Thr			
425	430	435	
ctccactcca cctccaccca ctgtccgcct ctgccccag agccccacgcc cgactagcag			1468
gcatgcccgcg gtaggttaagg gcccggac cgccgttagaga gcccggcccc ggacggacgt			1528
tggttctgca ctaaaaaccca tcttccccgg atgtgtgtct caccctctat cctttactt			1588
tttgccccctt ccactttgag taccaaatacc acaagccatt ttttggaggag agtggaaagag			1648

agtaccatgc tggcgccgca gagggaaaggg gcctacaccc gtcttggggc tegccccacc 1708
 cagggtcccc tcctggagca tcccaggccg cgcacgccaa cagccccccc cttgaatctg 1768
 cagggagcaa ctctccactc catatttatt taaacaattt ttccccaaa ggcatccata 1828
 gtgcactagc attttcttga accaataatg tattaaaatt ttttgatgtc agccttgcatt 1888
 caagggttt atcaaaaagt acaataataa atcctcaggt agtactggga atgaaaggct 1948
 ttgccatggg cctgctgcgt cagaccagta ctgggaagga ggacgggtgt aagcagttgt 2008
 tatttagtga tattgtgggt aacgtgagaa gatagaacaa tgctataata tataatgaac 2068
 acgtgggtat ttaataagaa acatgatgtg agattacttt gtcccgctta ttctccccc 2128
 tgttatctgc tagatctagt tctcaatcac tgctcccccg tgtgtattag aatgcatgt 2188
 aggtcttctt gtgtcctgat gaaaaatatg tgctgaaat gagaaacttt gatctctgt 2248
 tactaatgtg ccccatgtcc aagtccaaacc tgccctgtca tgacctgatc attacatggc 2308
 tgtggttccct aaggctgttg ctgaagtcatt tgtcgctcag caatagggtg cagtttcca 2368
 ggaataggca tttgctaatt cctggcatga cactcttagtg acttcctggt gaggcccagc 2428
 ctgtcctggt acagcagggt cttgctgtaa ctcagacatt ccaagggtat ggaaagccat 2488
 attcacacct cacgctctgg acatgatttta gggaaagcagg gacacccccc gccccccacc 2548
 tttggatca gcctccgcca ttccaagtca acactttct tgagcagacc gtgatttgg 2608
 agagaggcac ctgctggaaa ccacacttct tgaaacagcc tgggtgacgg tcctttaggc 2668
 agcctggccgc cgtctctgtc ccgggttacc ttgccgagag aggccgtct gccccaccct 2728
 caaacccctgt ggggcctgat ggtgctcag actcttcctg caaagggaac tgaagacctc 2788
 cacattaagt ggcttttaa cataaaaac acggcagctg tagctccga gctactct 2848
 tgccagcatt ttcacatttt gcctttctcg tggtagaagc cagtagcagag aaattctgt 2908
 gtggaaacat tcgaggtgtc accctgcaga gctatggta ggtgtggata aggcttaggt 2968
 gccaggctgt aagcattctg agctggctt tttttttaa gtcctgtata tgtatgttagt 3028
 agtttgggtg tgtatatata gtagcatttc aaaatggacg tactggtttta acctcctatc 3088
 cttggagagc agctggctct ccaccttgc acacattatg ttagagaggt agcgagctgc 3148
 tctgctatat gccttaagcc aatatttact catcaggtca ttatttttta caatggccat 3208
 ggaataaaacc atttttacaa aaataaaaac aaaaaaagc 3247

<210> 4
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
<223> PCR Primer

<400> 4
ggagttcgag cagatcgaca a

21

<210> 5
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 5
ggccactcta catgggaagt c

21

<210> 6
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Probe

<400> 6
agctgggcgg ccatttacca ggat

24

<210> 7.
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 7
gaagggtgaag gtcggagtc

19

<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 8
gaagatggtg atgggatttc

20

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
 <223> PCR Probe

<400> 9
 caagcttccc gttctcagcc 20

<210> 10
 <211> 4127
 <212> DNA
 <213> Rattus norvegicus

<220>
 <221> CDS
 <222> (120)...(1418)

<400> 10
 agccgctgct gggaggttg gggctgaggt ggtggcgggc gacgggcctc gagacgcgga 60
 gcgacgcggc ctagcgcggc ggacggccga ggaaactcg 60
 gcagtcgtcc cgtcccgcc 119

atg gaa atg gag aag gaa ttc gag cag atc gat aag gct ggg aac tgg 167
 Met Glu Met Glu Lys Glu Phe Glu Gln Ile Asp Lys Ala Gly Asn Trp
 1 5 10 15

gcg gct att tac cag gat att cga cat gaa gcc agt gac ttc cca tgc 215
 Ala Ala Ile Tyr Gln Asp Ile Arg His Glu Ala Ser Asp Phe Pro Cys
 20 25 30

aga ata gcg aaa ctt cct aag aac aaa aac cgg aac agg tac cga gat 263
 Arg Ile Ala Lys Leu Pro Lys Asn Lys Asn Arg Asn Arg Tyr Arg Asp
 35 40 45

gtc agc cct ttt gac cac agt cgg att aaa ttg cat cag gaa gat aat 311
 Val Ser Pro Phe Asp His Ser Arg Ile Lys Leu His Gln Glu Asp Asn
 50 55 60

gac tat atc aat gcc agc ttg ata aaa atg gag gaa gcc cag agg agc 359
 Asp Tyr Ile Asn Ala Ser Leu Ile Lys Met Glu Glu Ala Gln Arg Ser
 65 70 75 80

tat atc ctc acc cag ggc cct tta cca aac acg tgc ggg cac ttc tgg 407
 Tyr Ile Leu Thr Gln Gly Pro Leu Pro Asn Thr Cys Gly His Phe Trp
 85 90 95

gag atg gtg tgg gag cag aag agc agg ggc gtg gtc atg ctc aac cgc 455
 Glu Met Val Trp Glu Gln Lys Ser Arg Gly Val Val Met Leu Asn Arg
 100 105 110

atc atg gag aaa ggc tcg tta aaa tgt gcc cag tat tgg cca cag aaa 503
 Ile Met Glu Lys Gly Ser Leu Lys Cys Ala Gln Tyr Trp Pro Gln Lys
 115 120 125

gaa gaa aaa gag atg gtc ttc gat gac acc aat ttg aag ctg aca ctg 551
 Glu Glu Lys Glu Met Val Phe Asp Asp Thr Asn Leu Lys Leu Thr Leu
 130 135 140

atc tct gaa gat gtc aag tca tat tac aca gta cgg cag ttg gag ttg Ile Ser Glu Asp Val Lys Ser Tyr Tyr Thr Val Arg Gln Leu Glu Leu 145 150 155 160	599
gag aac ctg gct acc cag gag gct cga gag atc ctg cat ttc cac tac Glu Asn Leu Ala Thr Gln Glu Ala Arg Glu Ile Leu His Phe His Tyr 165 170 175	647
acc acc tgg cct gac ttt gga gtc cct gag tca cct gcc tct ttc ctc Thr Thr Trp Pro Asp Phe Gly Val Pro Glu Ser Pro Ala Ser Phe Leu 180 185 190	695
aat ttc cta ttc aaa gtc cga gag tca ggc tca ctc agc cca gag cac Asn Phe Leu Phe Lys Val Arg Glu Ser Gly Ser Leu Ser Pro Glu His 195 200 205	743
ggc ccc att gtg gtc cac tgc agt gct ggc att ggc agg tca ggg acc Gly Pro Ile Val Val His Cys Ser Ala Gly Ile Gly Arg Ser Gly Thr 210 215 220	791
ttc tgc ctg gct gac acc tgc ctc tta ctg atg gac aag agg aaa gag Phe Cys Leu Ala Asp Thr Cys Leu Leu Met Asp Lys Arg Lys Asp 225 230 235 240	839
ccg tcc tct gtg gac atc aag aaa gtg ctg ttg gag atg cgc agg ttc Pro Ser Ser Val Asp Ile Lys Lys Val Leu Leu Glu Met Arg Arg Phe 245 250 255	887
cgc atg ggg ctc atc cag acg gcc gac caa ctg cgc ttc tcc tac ctg Arg Met Gly Leu Ile Gln Thr Ala Asp Gln Leu Arg Phe Ser Tyr Leu 260 265 270	935
gct gtg atc gag ggt gca aag ttc atc atg ggc gac tcg tca gtg cag Ala Val Ile Glu Gly Ala Lys Phe Ile Met Gly Asp Ser Ser Val Gln 275 280 285	983
gat cag tgg aag gag ctt tcc cat gaa gac ctg gag cct ccc cct gag Asp Gln Trp Lys Glu Leu Ser His Glu Asp Leu Glu Pro Pro Pro Glu 290 295 300	1031
cac gtg ccc cca cct ccc cgg cca ccc aaa cgc aca ttg gag cct cac His Val Pro Pro Pro Pro Arg Pro Pro Lys Arg Thr Leu Glu Pro His 305 310 315 320	1079
aat ggc aag tgc aag gag ctc ttc aac cac cag tgg gtg agc gag Asn Gly Lys Cys Lys Glu Leu Phe Ser Asn His Gln Trp Val Ser Glu 325 330 335	1127
gag agc tgt gag gag gac atc ctg gcc aga gag gaa agc aga gcc Glu Ser Cys Glu Asp Glu Asp Ile Leu Ala Arg Glu Glu Ser Arg Ala 340 345 350	1175
ccc tca att gct gtg cac agc atg agt atg agt caa gac act gaa Pro Ser Ile Ala Val His Ser Met Ser Ser Met Ser Gln Asp Thr Glu 355 360 365	1223
gtt agg aaa cgg atg gtg ggt gga ggt ctt caa agt gct cag gca tct Val Arg Lys Arg Met Val Gly Gly Gly Leu Gln Ser Ala Gln Ala Ser 370 375 380	1271

gtc ccc act gag gaa gag ctg tcc cca acc gag gag gaa caa aag gca 1319
 Val Pro Thr Glu Glu Glu Leu Ser Pro Thr Glu Glu Glu Gln Lys Ala
 385 390 395 400
 cac agg cca gtt cac tgg aag ccc ttc ctg gtc aac gtg tgc atg gcc 1367
 His Arg Pro Val His Trp Lys Pro Phe Leu Val Asn Val Cys Met Ala
 405 410 415
 acg gcc ctg gcg act ggc gcg tac ctc tgt tac cgg gta tgt ttt cac 1415
 Thr Ala Leu Ala Thr Gly Ala Tyr Leu Cys Tyr Arg Val Cys Phe His
 420 425 430
 tga cagactgctg tgagggcatga gcgtgggtggg cgctgccact gcccaggta 1468

 ggatttggtc tgccggcgtct aacctggtgt agaagaaaaca acagcttaca agcctgtgg 1528
 ggaactggaa gggccagccc caggaggggc atctgtgcac tgggcttga aggagcccc 1588
 ggtcccaaga acagagtcta atctcaggc cttaacctgt tcaggagaag tagaggaaat 1648
 gccaaatact cttcttgctc tcacctcaact cctccccc ttctggttcg tttgttttg 1708
 gaaaaaaaaaaa aaaaagaatt acaacacatt gttgtttta acatttataa aggcaggttt 1768
 ttgttatttt tagagaaaaac aaaagatgtc aggcactggt gagattctct tgccttgc 1828
 ggcatgtgat cagattcacg attacgttt atttccgggg gagggtccca cttgtcagga 1888
 ctgtaaagtt cttgtggct tggcagccc ccccaccccc ccaccccgag cttgcagggt 1948
 ccctgctgtg aggagagcag cagcagaggc tgccctgga cagaagccca gctctgttc 2008
 cttcagggtt ccctgcgtt ccatccctt tcttgcac cgccatctt cagatgaccc 2068
 agtcctcagc accccacccc tgcagatggg tttctccgag ggcctgcctc agggtcatca 2128
 gaggttggct gccagcttag agctggggct tccatttgat tggaaagtca ttactattct 2188
 atgtagaagc cactccactg aggtgtaaag caagactcat aaaggaggag cttgggtgtc 2248
 atggaaagtca ctccgcgcgc aggacctgta acaacactctg aaacactcag tcctgctgca 2308
 gtgacgtcct tgaaggcatc agacagatga tttgcagact gccaagactt gtcctgagcc 2368
 gtgattttta gagtctggac tcatgaaaca ccggccgagcg cttactgtgc agcctctgat 2428
 gctgggtggc tgaggctgag gggaggtgga cactgtgggt gcatccagtg cagttgttt 2488
 tgtgcagttt ggtccagcag cacagccgc actccagcct cagctgcagg ccacagtggc 2548
 catggaggcc gccagagcga gctggggtgg atgcttgcactt acggagcata gcttcccg 2608
 gacgtgcagc tcccttcctg ctttgcctt ctgcttcctt ccctggagta gcaagccac 2668
 gagcaatcgt gaggggtgtg agggagctgc agaggcatca gagtggcctg cagcggcgtg 2728
 agcccccttc ccctccgaca ccccccctcca gaggagccgc tccactgtta tttattcact 2788

ttgcccacag acacccctga gtgagcacac cctgaaactg accgtgtaaag gtgtcagcct 2848
 gcacccagga ccgtcagggtg cagcacccggg tcagtcctag gggtgaggta ggactgacac 2908
 agccactgtg tggctggtgc tggggcaggg gcaggagctg agggtcttag aagcaatatt 2968
 caggaacaga caacagtggt gacatgtaaa gtcctgtgg ctactgtatca catgtgtagg 3028
 atgaaggctg gcctttctcc catgacttcc tagatcccgt tccccgtctg cttccctgt 3088
 gagttagaaa acacacaggc tcctgtcctg gtgggtccgt gtgcttgaca tggaaactt 3148
 agatgcctgc tcactggcg gcacccggc atcggccacca ctcagagtga gagcagtgt 3208
 gtccagtgcc gaggccgcct gactcccgcc aggactcttc aggctctggc ctgccccagc 3268
 acaccccgct gnatctcaga cattccacac ccacaccta ttccctggac acttggcaa 3328
 gcaggccccgc cttccacact ctggggtcag cccctccatt ccgagttcac actgctctgg 3388
 agcaggccag gaccggaaagc aaggcagctg gtgaggagca ccctcctggg aacagtgtag 3448
 gtgacagtcc tgagagtcag ctgtctcg ctgtggcac cagtcacctt gtcagaagt 3508
 gtgtggctct tgaggctgaa gagactgtatg atgggtctca tgactcttct gtgagggaa 3568
 cttgacccctt acattgggtg gctttttta aaataagcga aggtagctgg aactccagtc 3628
 tgcctcttc cagcacttca cattttgcct ttccacccaga gaagccagca cagagccact 3688
 ggggaaggcg atggccttgc ctgcacaggg tgaggagatg gtcagccgg cgtccaggct 3748
 gtgtctggag caggggggtgc acaggcgcct cacaggtggg ggcctcagag caggcgctgc 3808
 cctgtccctt gccccgtctgg aggcagcaaa gtcgtgcatt gccttaagtc aataacttact 3868
 cagcaggccgc ctctcgttct ctctctctct ctctctctct ctctctctct 3928
 ctctctaaat ggccatagaa taaaccattt tacaaaaata aaagccaaca acaaagtgt 3988
 ctggaatagc acctttgcag gagcgggggg tgcgtcaggg tcttctgtga cctcaccgaa 4048
 ctgtccgact gcaccgtttc caacttgtgt ctactaatg ggtctgcatt agttgcaaca 4108
 ataaatgttt taaaagaac 4127

<210> 11
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR Primer

<400> 11
 cgagggtgca aagtccatca t

<210> 12
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 12
ccaggtcttc atggaaaggc t

21

<210> 13
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Probe

<400> 13
cgactcgta gtgcaggatc agtggaa

26

<210> 14
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 14
tgttcttagag acagccgcat ctt

23

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 15
caccgacctt caccatcttg t

21

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Probe

<400> 16
tttgtcagtg ccagcctcgt ctca

24

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 17
cttagccccc aggccccccc

20

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 18
ctcggcccac tgcgcgtct

20

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 19
catgacgggc cagggcggct

20

<210> 20
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 20
cccgacttg tcgatctgct

20

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 21
ctggcttcat gtcggatatac

20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 22
ttggccactc tacatgggaa

20

<210> 23
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 23
ggactgacgt ctctgtacct

20

<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 24
gatgttagttt aatccgacta

20

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 25
ctagcgttga tatagtcatt

20

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 26
gggttaagaat gtaactcctt

20

<210> 27
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 27
tgaccgcatg tggtaggcaa

20

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 28
ttttctgctc ccacaccatc

20

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 29
ctctgtttag catgacgaca

20

<210> 30
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 30
gcgcattttt acgaaccttt

20

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 31
aaatttgtt cttcaaagat

20

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 32
tgatatcttc agagatcaat

20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 33
tctagctgtc gcactgtata

20

<210> 34
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 34
agtttcttgg gttgtaagg

20

<210> 35
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 35
gtggtatagt ggaaatgtaa

20

<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 36
tgattcaggg actccaaagt

20

<210> 37
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 37 20
ttgaaaagaaa agttcaagaa

<210> 38
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 38 20
gggctgagtg accctgactc

<210> 39
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 39 20
gcagtgcacc acaacgggcc

<210> 40
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 40 20
aggcccgaga cctgccatg

<210> 41
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 41 20
agcaggaggc aggtatcagc

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 42
gaagaagggt ctttcctctt

20

<210> 43
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 43
tctaacagca ctttcattgat

20

<210> 44
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 44
atcaacccca tccgaaactt

20

<210> 45
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 45
gagaagcgca gctggtcggc

20

<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 46
tttggcacct tcgatcacag

20

<210> 47
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 47
agctccttcc actgatcctg

20

<210> 48
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 48
tccaggattc gtttgggtgg

20

<210> 49
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 49
gaactccctg catttcccat

20

<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 50
ttccttcacc cactggtgat

20

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 51
gttaggtgcg gcatttaagg

20

<210> 52
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 52
cagtgtcttg actcatgctt

20

<210> 53
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 53
gcctggcac ctcgaagact

20

<210> 54
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 54
ctcgcccttc tcgggcagtg

20

<210> 55
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 55
gggcttccag taactcagtg

20

<210> 56
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 56
ccgtagccac gcacatgttg

20

<210> 57
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 57
tagcagaggt aagcgccggc

20

<210> 58
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 58
ctatgtttg ctgttgaaca

20

<210> 59
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 59
ggaggtggag tggaggaggg

20

<210> 60
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 60
ggctctgcgg gcagaggcgg

20

<210> 61
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 61
ccgcggcatg cctgctagtc

20

<210> 62
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 62
tctctacgcg gtcggcgcc 20

<210> 63
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 63
aagatgggtt tttagtgcaga 20

<210> 64
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 64
gtactctctt tcactctcct 20

<210> 65
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 65
ggcccccattcc ctctgcgcgg 20

<210> 66
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 66
ctccaggagg gagccctggg 20

<210> 67
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 67
gggctgttgg cgtgcgcgc

20

<210> 68
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 68
tttaaataaa tatggagtgg

20

<210> 69
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 69
gttcaagaaa atgctagtgc

20

<210> 70
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 70
ttgataaaaggc ccttgatgca

20

<210> 71
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 71
atggcaaaggc cttccattcc

20

<210> 72
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 72
gtcctccatcc ccagttactgg

20

<210> 73
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 73
ttacccacaa tatcaactaaa

20

<210> 74
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 74
attatatatt atagcattgt

20

<210> 75
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 75
tcacatcatg tttcttattta

20

<210> 76
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 76
ataacaggga ggagaataag

20

<210> 77
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 77
ttacatgcac tctaatacac
.

20

<210> 78
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 78
gatcaaagg tt tctcatttca

20

<210> 79
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 79
ggtcatgcac aggcagggtt

20

<210> 80
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 80
caacaggctt aggaaccaca

20

<210> 81
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 81
aactgcaccc tattgctgag

20

<210> 82
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 82
gtcatgccag gaatttagcaa

20

<210> 83
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 83
acaggctggg cctcaccagg

20

<210> 84
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 84
tgagttacag caagaccctg

20

<210> 85
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 85
gaatatggct tcccataccc

20

<210> 86
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 86
ccctaaatca tgtccagagc

20

<210> 87
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 87
gactttggaaat ggccggaggct

20

<210> 88
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 88
caaattcacgg tctgctcaag

20

<210> 89
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 89
gaagtgtggc ttccagcagg

20

<210> 90
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 90
cctaaaggac cgtcacccag

20

<210> 91
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 91
gtgaacctggg acagagacgg

20

<210> 92
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 92
gccccacagg gtttgggggt

20

<210> 93
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 93
cctttgcagg aagagtctgtg

20

<210> 94
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 94
aaagccacctt aatgtggagg

20

<210> 95
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 95
gtaaaaatgc tggcaagaga

20

<210> 96
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 96
tcagaatgct tacaggctgg

20

<210> 97
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 97
caacctcccc agcagcggct 20

<210> 98
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 98
tcgaggcccg tcgcccgc 20

<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 99
cctcggccgt ccggcgcgat 20

<210> 100
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 100
tcgatctgct cgaattcctt 20

<210> 101
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 101
cctggtaaat agccgccccag 20

<210> 102
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 102
tgtcgaatat cctggtaaat

20

<210> 103
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 103
actggcttca tgtcgaatat

20

<210> 104
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 104
aagtcaactgg cttcatgtcg

20

<210> 105
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 105
gaagtcaactg gttcatgtc

20

<210> 106
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 106
ggaagtcaact ggttcatgt

20

<210> 107
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 107
gggaagtca tggcttcatg

20

<210> 108
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 108
tggaaagtca ctggcttcat

20

<210> 109
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 109
atgggaagtc actggcttc

20

<210> 110
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 110
catgggaagt cactggcttc

20

<210> 111
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 111
tttttgttct taggaagttt

20

<210> 112
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 112
cggttttgt tcttaggaag

20

<210> 113
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 113
tccgactgtg gtcaaaaggg

20

<210> 114
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 114
ttaatccgac tgtggtcaa

20

<210> 115
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 115
atagtcatta tcttcctgat

20

<210> 116
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 116
ttgatatagt cattatctc

20

<210> 117
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 117
gcttcctccca ttttatcaa

20

<210> 118
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 118
ggccctgggt gaggatata

20

<210> 119
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 119
cacaccatct cccagaagt

20

<210> 120
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 120
tgctcccaca ccatctcccc

20

<210> 121
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 121
ctgctcccac accatctccc

20

<210> 122
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 122 20
tctgctccca caccatctcc

<210> 123
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 123 20
ttctgctccc acaccatctc

<210> 124
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 124 20
ccccgtct tctgctccca

<210> 125
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 125 20
atgcgggtga gcatgaccac

<210> 126
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 126 20
tttaacgagc ctttctccat

<210> 127
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 127
tttttttctt tctgtggcca

20

<210> 128
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 128
gaccatctct ttttcttctt

20

<210> 129
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 129
tcagagatca gtgtcagctt

20

<210> 130
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 130
cttgacatct tcagagatca

20

<210> 131
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 131
taatatgact tgacatcttc

20

<210> 132
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 132
aactccaaact gccgtactgt

20

<210> 133
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 133
tctctcgagc ctcctgggta

20

<210> 134
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 134
ccaaagtcaag gccaggtgg

20

<210> 135
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 135
gggactccaa agtcaggcca

20

<210> 136
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 136
aggactccaa aagtcaaggcc

20

<210> 137
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 137 20
cagggactcc aaagttaggc

<210> 138
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 138 20
tcagggactc caaaatcgagg

<210> 139
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 139 20
ggtgactcag ggactccaaa

<210> 140
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 140 20
cctgactctc ggactttgaa

<210> 141
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 141 20
gctgagttag cctgactctc

<210> 142
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 142
ccgtgctctg ggctgagtga

20

<210> 143
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 143
aaggtccctg acctgccaat

20

<210> 144
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 144
tctttcctct tgcgtccatcag

20

<210> 145
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 145
gtctttcctc ttgtccatca

20

<210> 146
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 146
ggtctttcct cttgtccatc

20

<210> 147
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 147
gggtcttcc tcttgtccat

20

<210> 148
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 148
aacagcactt tcttgatgtc

20

<210> 149
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 149
ggaacctgcg catctccaac

20

<210> 150
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 150
tggteggccg tctggatgag

20

<210> 151
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 151
gagaagcgca gttggtcggc

20

<210> 152
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 152
agtaggaga agcgcgatgg

20

<210> 153
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 153
gccaggtagg agaagcgca

20

<210> 154
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 154
agccaggtag gagaagcgca

20

<210> 155
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 155
cagccaggta ggagaagcgc

20

<210> 156
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 156
acagccaggta aggagaagcg

20

<210> 157
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 157
cacagccagg taggagaagg
..

20

<210> 158
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 158
tcacagccag gtaggagaag

20

<210> 159
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 159
atcacagcca ggtaggagaa

20

<210> 160
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 160
gatcacagcc aggtaggaga

20

<210> 161
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 161
cgatcacagc caggtaggag

20

<210> 162
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 162
tcgatcacag ccaggttagga

20

<210> 163
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 163
caccctcgat cacagccagg

20

<210> 164
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 164
tccttccact gatcctgcac

20

<210> 165
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 165
ctccttccac tgatcctgca

20

<210> 166
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 166
gttccttcca ctgatcctgc

20

<210> 167
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 167
agctccttcc actgatccctg

20

<210> 168
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 168
aagctcccttc cactgatccct

20

<210> 169
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 169
aaagctcctt ccactgatcc

20

<210> 170
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 170
gaaagctctt tccactgatc

20

<210> 171
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 171
ggaaaagctccc ttccactgat

20

<210> 172
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 172
gggaaagctc cttccactga

20

<210> 173
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 173
tggaaaagct cttccactg

20

<210> 174
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 174
tggccgggga ggtgggggca

20

<210> 175
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 175
tgggtggccg gggaggtggg

20

<210> 176
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 176
tgcgtttggg tggccgggga

20

<210> 177
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 177
tgcacttgcc attgtgaggc
.

<210> 178
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 178
acttcagtgt cttgactcat
.

<210> 179
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 179
aacttcagtg tcttgactca
.

<210> 180
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 180
taacttcagt gtcttgactc
.

<210> 181
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 181
ctaacttcag tgtcttgact

20

20

20

20

20

<210> 182
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 182 20
gacagatgcc tgagcacttt

<210> 183
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 183 20
gaccaggaag ggcttccagt

<210> 184
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 184 20
tgaccagga gggcttccag

<210> 185
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 185 20
ttgaccagga agggcttcca

<210> 186
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 186 20
gttggaccagg aaggggcttcca

<210> 187
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 187 20
gcacacgttg accaggaagg

<210> 188
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 188 20
gaggtacgcg ccagtcgccca

<210> 189
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 189 20
tacccggtaa cagaggtacg

<210> 190
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 190 20
agtggaaaaca tacccggtaa

<210> 191
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 191 20
caaatcctaa cctgggcagt

<210> 192
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 192
ttccagttcc accacaggct

20

<210> 193
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 193
ccagtgcaca gatgcccctc

20

<210> 194
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 194
acaggttaag gccctgagat

20

<210> 195
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 195
gccttagcatc ttttgggg

20

<210> 196
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 196
aagccagcag gaactttaca

20

<210> 197
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 197
gggacacctg aggaaagcag

20

<210> 198
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 198
ggtcatctgc aagatggcg

20

<210> 199
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 199
gccaacctct gatgaccctg

20

<210> 200
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 200
tggaaggccc agctctaagg

20

<210> 201
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 201
tagtaatgac ttccaatca

20

<210> 202
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 202
tgagtc ttgc tttacac ctc

20

<210> 203
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 203
cctgcgcg gactgacttc

20

<210> 204
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 204
aggacgtcac tgcagcagga

20

<210> 205
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 205
tcaggacaag tcttggcagt

20

<210> 206
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 206
gaggctgcac agtaagcgct

20

<210> 207
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 207 20
tcagccaacc agcatcagag

<210> 208
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 208 20
acccacagtg tccacacctcc

<210> 209
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 209 20
agtgcgggct gtgctgctgg

<210> 210
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 210 20
cagctcgctc tggcggcctc

<210> 211
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 211 20
aggaaaggag ctgcacgtcc

<210> 212
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 212
ccctcacgat tgctcgtggg

20

<210> 213
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 213
cagtggagcg gtcctctgg

20

<210> 214
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 214
caggctgaca ctttacacgg

20

<210> 215
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 215
gtccttacctc aacccttagga

20

<210> 216
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 216
ctgcggccagc accagccaca

20

<210> 217
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 217
atggcttcta agaccctcag

20

<210> 218
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 218
ttacatgtca ccactgttgt

20

<210> 219
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 219
tacacatgtc atcagtagcc

20

<210> 220
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 220
ttttctaact cacagggaaa

20

<210> 221
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 221
gtgcccggcca gtgagcaggc

20

<210> 222
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 222 20
cggcctcgac actggacagc

<210> 223
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 223 20
gtgaaatgtc tgagatccag

<210> 224
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 224 20
aggcgccgc tgcttgccca

<210> 225
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 225 20
cggtcctggc ctgctccaga

<210> 226
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 226 20
tacactgttc ccaggagggt

<210> 227
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 227
tggtgccagc agcgcttagca 20

<210> 228
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 228
cagtcctttc agcctcaaga 20

<210> 229
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 229
aagagtcatg agcaccatca 20

<210> 230
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 230
tgaaggtaa gttccccctca 20

<210> 231
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 231
ctggcaagag gcagactggaa 20

<210> 232
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 232
ggctctgtgc tggcttctct 20

<210> 233
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 233
gccatctcct cagcctgtgc 20

<210> 234
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 234
agcgccctgct ctgaggcccc 20

<210> 235
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

④ <400> 235
tgctgagtaa gtattgactt 20

<210> 236
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 236
ctatggccat ttagagagag 20

<210> 237
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 237
tggtttattc tatggccatt

20

<210> 238
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 238
cgctcctgca aaggtgctat

20

<210> 239
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 239
gttggaaacg gtgcagtccgg

20

<210> 240
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 240
atttattgtt gcaactaatg

20

<210> 241
<211> 2346
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (710)...(2008)

<400> 241
gaattcggga tcctttgca cattcctagt tagcagtgca tactcatcag actggagatg 60

ttaatgaca tcagggAACCA aaacggacAA cccatAGTAC ccgaAGACAG ggtGAACCAG 120
acaatcgtaa gcttGATGGT gtttCCCTG actGGGTAGT tgaAGCATCT catGAATGTC 180
agccaaATTC cgtacAGTTC ggtGCGGATC cgaACGAAAC acctCCCTGTA ccaggTTCCC 240
gtgtcgctct caatttcaat cagtcatct atttGTTGG gagTCTTGAT tttatTTacc 300
gtgaagacct tctctggctg gccccgggct ctcatgttgg tgtcatgaat taacttcaga 360
atdatccagg cttcatcatg tttcccacc tccagcaaga accgagggct ttctggcatg 420
aaggtagagag ccaccacaga ggagacgcat gggagcgcac agacgatgac gaagacgcgc 480
cacgtgtgga actggtaggc tgaacccatg ctgaagctcc acccgttagtg gggaatgatg 540
gcccaggcat ggcggaggct agatGCCGCC aatcatccag aacatgcaga agccgctgtc 600
ggggagcttgggctg ggtggcggt gacgggcTTc gggacgcgga ggcacgcggc 660
ctagcgcggc ggacggccgt ggaaactcgg gcagccgacc cgtccccGCC atg gag atg 718

Met Glu Met

1

gag aag gag ttc gag gag atc gac aag gct ggg aac tgg gcg gct att 766
Glu Lys Glu Phe Glu Glu Ile Asp Lys Ala Gly Asn Trp Ala Ala Ile
5 10 15

5

10

15

tac cag gac att cga cat gaa gcc agc gac ttc cca tgc aaa gtc gcg 814
 Tyr Gln Asp Ile Arg His Glu Ala Ser Asp Phe Pro Cys Lys Val Ala
 20 25 30 35

20

25

30

35

aag ctt cct aag aac aaa aac cg^g aac agg tac cga gat gtc agc cct 862
 Lys Leu Pro Lys Asn Lys Asn Arg Asn Arg Tyr Arg Asp Val Ser Pro
 40 45 50

40

45

30

ttt gac cac agt cg^g att aaa ttg cac cag gaa gat aat gac tat atc 910
 Phe Asp His Ser Arg Ile Lys Leu His Gln Glu Asp Asn Asp Tyr Ile
 55 60 65

55

60

65

70

75

80

acc cag ggc cct tta cca aac aca tgt ggg cac ttc tgg gag atg gtg 1006

Thr Gln Gly Pro Leu Pro Asn Thr Cys Gly His Phe Trp Glu Met Val
 85 90 95
 tgg gag cag aag agc agg ggc gtg gtc atg ctc aac cgc atc atg gag 1054
 Trp Glu Gln Lys Ser Arg Gly Val Val Met Leu Asn Arg Ile Met Glu
 100 105 110 115
 aaa ggc tcg tta aaa tgt gcc cag tat tgg cca cag caa gaa gaa aag 1102
 Lys Gly Ser Leu Lys Cys Ala Gln Tyr Trp Pro Gln Gln Glu Glu Lys
 120 125 130
 gag atg gtc ttt gat gac aca ggt ttg aag ttg aca cta atc tct gaa 1150
 Glu Met Val Phe Asp Asp Thr Gly Leu Lys Leu Thr Leu Ile Ser Glu
 135 140 145
 gat gtc aag tca tat tac aca gta cga cag ttg gag ttg gaa aac ctg 1198
 Asp Val Lys Ser Tyr Tyr Thr Val Arg Gln Leu Glu Leu Glu Asn Leu
 150 155 160
 act acc aag gag act cga gag atc ctg cat ttc cac tac acc aca tgg 1246
 Thr Thr Lys Glu Thr Arg Glu Ile Leu His Phe His Tyr Thr Thr Trp
 165 170 175
 cct gac ttt gga gtc ccc gag tca ccg gct tct ttc ctc aat ttc ctt 1294
 Pro Asp Phe Gly Val Pro Glu Ser Pro Ala Ser Phe Leu Asn Phe Leu
 180 185 190 195
 ttc aaa gtc cga gag tca ggc tca ctc agc ctg gag cat ggc ccc att 1342
 Phe Lys Val Arg Glu Ser Gly Ser Leu Ser Leu Glu His Gly Pro Ile
 200 205 210
 gtg gtc cac tgc agc gcc ggc atc ggg agg tca ggg acc ttc tgt ctg 1390
 Val Val His Cys Ser Ala Gly Ile Gly Arg Ser Gly Thr Phe Cys Leu
 215 220 225
 gct gac acc tgc ctc tta ctg atg gac aag agg aaa gac cca tct tcc 1438
 Ala Asp Thr Cys Leu Leu Leu Met Asp Lys Arg Lys Asp Pro Ser Ser
 230 235 240

gtg gac atc aag aaa gta ctg ctg gag atg cgc agg ttc cgc atg ggg 1486
 Val Asp Ile Lys Lys Val Leu Leu Glu Met Arg Arg Phe Arg Met Gly
 245 250 255

ctc atc cag act gcc gac cag ctg cgc ttc tcc tac ctg gct gtc atc 1534
 Leu Ile Gln Thr Ala Asp Gln Leu Arg Phe Ser Tyr Leu Ala Val Ile
 260 265 270 275

gag ggc gcc aag ttc atc atg ggc gac tcg tca gtg cag gat cag tgg 1582
 Glu Gly Ala Lys Phe Ile Met Gly Asp Ser Ser Val Gln Asp Gln Trp
 280 285 290

aag gag ctc tcc cgg gag gat cta gac ctt cca ccc gag cac gtg ccc 1630
 Lys Glu Leu Ser Arg Glu Asp Leu Asp Leu Pro Pro Glu His Val Pro
 295 300 305

cca cct ccc cgg cca ccc aaa cgc aca ctg gag cct cac aac ggg aag 1678
 Pro Pro Pro Arg Pro Pro Lys Arg Thr Leu Glu Pro His Asn Gly Lys
 310 315 320

tgc aag gag ctc ttc tcc agc cac cag tgg gtg agc gag gag acc tgt 1726
 Cys Lys Glu Leu Phe Ser Ser His Gln Trp Val Ser Glu Glu Thr Cys
 325 330 335

ggg gat gaa gac agc ctg gcc aga gag gaa ggc aga gcc cag tca agt 1774
 Gly Asp Glu Asp Ser Leu Ala Arg Glu Glu Gly Arg Ala Gln Ser Ser
 340 345 350 355

gcc atg cac agc gtg agc agc atg agt cca gac act gaa gtt agg aga 1822
 Ala Met His Ser Val Ser Ser Met Ser Pro Asp Thr Glu Val Arg Arg
 360 365 370

cgg atg gtg ggt gga ggt ctt caa agt gct cag gcg tct gtc ccc acc 1870
 Arg Met Val Gly Gly Leu Gln Ser Ala Gln Ala Ser Val Pro Thr
 375 380 385

gag gaa gag ctg tcc tcc act gag gag gaa cac aag gca cat tgg cca 1918
 Glu Glu Glu Leu Ser Ser Thr Glu Glu Glu His Lys Ala His Trp Pro
 390 395 400

agt cac tgg aag ecc ttc ctg gtc aat gtg tgc atg gcc acg ctc ctg 1966
Ser His Trp Lys Pro Phe Leu Val Asn Val Cys Met Ala Thr Leu Leu
405 410 415

gcc acc ggc gcg tac ttg tgc tac cgg gtg tgt ttt cac tga 2008
Ala Thr Gly Ala Tyr Leu Cys Tyr Arg Val Cys Phe His *
420 425 430

cagactggga ggcactgccca ctgcccagct taggatgcgg tctgcggcgt ctgacccgtt 2068
gttagaggaa caacaactcg caagcctgt ctggaaactgg aagggcctgc cccaggaggg 2128
tattagtgc a ctgggctttg aaggagcccc tggtcccacg aacagagttt aatctcaggg 2188
ccttaacctg ttcaaggagaa gtagaggaaa tgccaaatac tcttcttgct ctcacccac 2248
tcctccctt tctctgattt atttgtttt ggaaaaaaaaaaaaaaaagaa ttacaacaca 2308
ttgttggttt taacatttat aaaggcaggc ccgaattc 2346

<210> 242

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221> unsure

<222> (1)...(20)

<223> Antisense Oligonucleotide

<400> 242

nnnnnnnnnn nnnnnnnnnn

20